



SUBSTITUTE SEQUENCE LISTING

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<120> EXTENDED CDNAS FOR SECRETED PROTEINS

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<140> 09/663,600

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<151> 1998-11-13

<150> 60/066,677

<151> 1997-11-13

<150> 60/069,957

<151> 1997-12-17

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47

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 atcaagaatt cgcacgagac catta 25

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 taatggctctc gtgcgaattc ttgat 25

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 tcaccagcag gcagtggctt aggag 25

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 atgggaaagg aaaagactca tatca 25

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 tttttvn 67


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ccagcagagt cacgagagag actacacgg                                     29

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cacgagagag actacacggg actgg                                       25

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aatatrarac agctacaata ttccagggcc artcacttgc cattttctcat aacagcgtca      60
gagagaaaga actgactgar acgtttgag atg aag aaa gtt ctc ctc ctg atc      113
                               Met Lys Lys Val Leu Leu Leu Ile
                               -15                               -10

aca gcc atc ttg gca gtg gct gtw ggt ttc cca gtc tct caa gac cag      161
Thr Ala Ile Leu Ala Val Ala Val Gly Phe Pro Val Ser Gln Asp Gln
                               -5                               1                               5

gaa cga gaa aaa aga agt atc agt gac agc gat gaa tta gct tca ggr      209
Glu Arg Glu Lys Arg Ser Ile Ser Asp Ser Asp Glu Leu Ala Ser Gly
                               10                               15                               20

wtt ttt gtg ttc cct tac cca tat cca ttt cgc cca ctt cca cca att      257

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Xaa	Phe	Val	Phe	Pro	Tyr	Pro	Tyr	Pro	Phe	Arg	Pro	Leu	Pro	Pro	Ile	
25						30				35						
cca	ttt	cca	aga	ttt	cca	tgg	ttt	aga	cgt	aan	ttt	cct	att	cca	ata	305
Pro	Phe	Pro	Arg	Phe	Pro	Trp	Phe	Arg	Arg	Xaa	Phe	Pro	Ile	Pro	Ile	
40				45					50				55			
cct	gaa	tct	gcc	cct	aca	act	ccc	ctt	cct	agc	gaa	aag	taaacaaraa			354
Pro	Glu	Ser	Ala	Pro	Thr	Thr	Pro	Leu	Pro	Ser	Glu	Lys				
			60					65								
ggaaaagtca	crataaacct	ggtcacctga	aattgaaatt	gagccacttc	cttgaaraat											414
caaaattcct	gttaataaaa	raaaaacaaa	tgtaattgaa	atagcacaca	gcatttctcta											474
gtcaatatct	ttagtgatct	tctttaataa	acatgaaagc	aaaaaaaaaa	aa											526

<210> 18
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 <221> SIGNAL
 <222> 1..17
 <223> Von Heijne matrix
 score 8.2
 seq LLLITAILAVAVG/FP

<400> 18
 Met Lys Lys Val Leu Leu Leu Ile Thr Ala Ile Leu Ala Val Ala Val
 1 5 10 15
 Gly

<210> 19
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 <212> DNA
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134


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<222> 346..408
<223> Von Heijne matrix
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<222> 115
<223> n=a, g, c or t
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actccttttta gcataggggc ttcggcgcca gcggccagcg ctagtcgggc tggtaagtgc      60
ctgatgccga gttccgtctc tcgcgtcttt tcctgggtccc aggcaaagcg gasgnagatc      120
ctcaaacggc ctagtgcttc gcgcttccgg agaaaatcag cggtctaatt aattcctctg      180
gtttgttgaa gcagttacca agaattctca accctttccc acaaaagcta attgagtaca      240
cgttcctggt gagtacacgt tcctgttgat ttacaaaagg tgcaggtatg agcaggtctg      300
aagactaaca ttttgtgaag ttgtaaaaca gaaaacctgt tagaa atg tgg tgg ttt      357
                                         Met Trp Trp Phe
                                         -20
cag caa ggc ctc agt ttc ctt cct tca gcc ctt gta att tgg aca tct      405
Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val Ile Trp Thr Ser
      -15                      -10                      -5
gct gct ttc ata ttt tca tac att act gca gta aca ctc cac cat ata      453
Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr Leu His His Ile
      1                      5                      10                      15
gac ccg gct tta cct tat atc agt gac act ggt aca gta gct cca raa      501
Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr Val Ala Pro Xaa
      20                      25                      30
aaa tgc tta ttt ggg gca atg cta aat att gcg gca gtt tta tgt caa      549
Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala Val Leu Cys Gln
      35                      40                      45
aaa tagaaatcag gaarataatt caacttaaag aakttcattt catgaccaa      602
Lys
ctcttcaraa acatgtcttt acaagcatat ctcttgtatt gctttctaca ctggttgaatt      662
gtctggcaat atttctgcag tggaaaattt gatttarmta gttcttgact gataaatatg      722
gtaaggtggg cttttccccc tgtgttaattg gctactatgt cttactgagc caagttgtaw      782
tttgaaataa aatgatatga gagtgacaca aaaaaaaaaa      822

<210> 20
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<212> PRT
<213> Homo Sapiens
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<221> SIGNAL
<222> 1..21
<223> Von Heijne matrix
      score 5.5

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      seq SFLPSALVIWTSA/AF
<400> 20
Met Trp Trp Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val
1           5           10           15
Ile Trp Thr Ser Ala
      20

<210> 21
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<212> DNA
<213> Homo Sapiens
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<222> complement(103..398)
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<221> sig_peptide
<222> 185..295
<223> Von Heijne matrix
<400> 21
atcaccttct tctccatcct tstctggggcc agtccccarc ccagtccctc tcctgacctg      60
cccagcccaa gtcagccttc agcacgcgct tttctgcaca cagatatgcc aggcctacct      120
ggcattccag gacctccgma atgatgctcc agtcccttac aagcgcttcc tggatgaggg      180
tggc atg gtg ctg acc acc ctc ccc ttg ccc tct gcc aac agc cct gtg      229
      Met Val Leu Thr Thr Leu Pro Leu Pro Ser Ala Asn Ser Pro Val
            -35           -30           -25
aac atg ccc acc act ggc ccc aac agc ctg agt tat gct agc tct gcc      277
Asn Met Pro Thr Thr Gly Pro Asn Ser Leu Ser Tyr Ala Ser Ser Ala
            -20           -15           -10
ctg tcc ccc tgt ctg acc gct cca aak tcc ccc cgg ctt gct atg atg      325
Leu Ser Pro Cys Leu Thr Ala Pro Xaa Ser Pro Arg Leu Ala Met Met
            -5           1           5           10
cct gac aac taaatatacct tatccaaatc aataaarwra raatcctccc      374
Pro Asp Asn
tccaraaggg tttctaaaaa caaaaaaaaaa a      405

<210> 22
<211> 37
<212> PRT
<213> Homo Sapiens
<220>
<221> SIGNAL
<222> 1..37
<223> Von Heijne matrix
      score 5.9
      seq LSYASSALSPCLT/AP
<400> 22
Met Val Leu Thr Thr Leu Pro Leu Pro Ser Ala Asn Ser Pro Val Asn
1           5           10           15
Met Pro Thr Thr Gly Pro Asn Ser Leu Ser Tyr Ala Ser Ser Ala Leu
      20           25           30
Ser Pro Cys Leu Thr
      35

<210> 23
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<212> DNA
<213> Homo Sapiens

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7 B6


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<222> 101
<223> n=a, g, c or t
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attagccgtg gcctaggccg tttaacgggg tgacacgagc ntgcagggcc gagtccaagg      120
cccggagata ggaccaaccg tcaggaatgc gaggaatgtt tttcttcgga ctctatcgag      180
gcacacagac agacc atg ggg att ctg tct aca gtg aca gcc tta aca ttt      231
                Met Gly Ile Leu Ser Thr Val Thr Ala Leu Thr Phe
                -15                -10                -5

gcc ara gcc ctg gac ggc tgc aga aat ggc att gcc cac cct gca agt      279
Ala Xaa Ala Leu Asp Gly Cys Arg Asn Gly Ile Ala His Pro Ala Ser
                1                5                10

gag aag cac aga ctc gag aaa tgt agg gaa ctc gag asc asc cac tcg      327
Glu Lys His Arg Leu Glu Lys Cys Arg Glu Leu Glu Xaa Xaa His Ser
                15                20                25

gcc cca gga tca acc cas cac cga aga aaa aca acc aga aga aat tat      375
Ala Pro Gly Ser Thr Xaa His Arg Arg Lys Thr Thr Arg Arg Asn Tyr
                30                35                40                45

tct tca gcc tgaaatgaak ccgggatcaa atggttgctg atcaragccc      424
Ser Ser Ala
atattttaaat tggaaaagtc aaattgasca ttattaaata aagcttgttt aatatgtctc      484
aaacaaaaaa aa      496

<210> 24
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<212> PRT
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<221> SIGNAL
<222> 1..15
<223> Von Heijne matrix
        score 5.5
        seq ILSTVTALTFAXA/LD
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<221> UNSURE
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Met Gly Ile Leu Ser Thr Val Thr Ala Leu Thr Phe Ala Xaa Ala
1                5                10                15

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137


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                                         Met Glu Arg
                                         -15
ctc gtc cta acc ctg tgc acc ctc ccg ctg gct gtg gcg tct gct ggc      105
Leu Val Leu Thr Leu Cys Thr Leu Pro Leu Ala Val Ala Ser Ala Gly
-10 -5 1
tgc gcc acg acg cca gct cgc aac ctg agc tgc tac cag tgc ttc aag      153
Cys Ala Thr Thr Pro Ala Arg Asn Leu Ser Cys Tyr Gln Cys Phe Lys
5 10 15
gtc agc agc tgg acg gag tgc ccg ccc acc tgg tgc agc ccg ctg gac      201
Val Ser Ser Trp Thr Glu Cys Pro Pro Thr Trp Cys Ser Pro Leu Asp
20 25 30 35
caa gtc tgc atc tcc aac gag gtg gtc gtc tct ttt aaa tgg agt gta      249
Gln Val Cys Ile Ser Asn Glu Val Val Val Ser Phe Lys Trp Ser Val
40 45 50
cgc gtc ctg ctc agc aaa cgc tgt gct ccc aga tgt ccc aac gac aac      297
Arg Val Leu Leu Ser Lys Arg Cys Ala Pro Arg Cys Pro Asn Asp Asn
55 60 65
atg aak ttc gaa tgg tgc ccg gcc ccc atg gtg caa ggc gtg atc acc      345
Met Xaa Phe Glu Trp Ser Pro Ala Pro Met Val Gln Gly Val Ile Thr
70 75 80
agg cgc tgc tgt tcc tgg gct ctc tgc aac agg gca ctg acc cca cag      393
Arg Arg Cys Cys Ser Trp Ala Leu Cys Asn Arg Ala Leu Thr Pro Gln
85 90 95
gag ggg cgc tgg gcc ctg cra ggg ggg ctc ctg ctc cag gac cct tcg      441
Glu Gly Arg Trp Ala Leu Xaa Gly Gly Leu Leu Leu Gln Asp Pro Ser
100 105 110 115
agg ggc ara aaa acc tgg gtg cgg cca cag ctg ggg ctc cca ctc tgc      489
Arg Gly Xaa Lys Thr Trp Val Arg Pro Gln Leu Gly Leu Pro Leu Cys
120 125 130
ctt ccc awt tcc aac ccc ctc tgc cca rgg gaa acc cag gaa gga      534
Leu Pro Xaa Ser Asn Pro Leu Cys Pro Xaa Glu Thr Gln Glu Gly
135 140 145
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taaactctca tgcccccaaa aaaaaaaaaa      623

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                                Met Leu Trp Leu Leu Phe Phe
                                -10
ctg gtg act gcc att cat gct gaa ctc tgt caa cca ggt gca gaa aat      100
Leu Val Thr Ala Ile His Ala Glu Leu Cys Gln Pro Gly Ala Glu Asn
                                -5              1              5
gct ttt aaa gtg aga ctt agt atc aga aca gct ctg gga gat aaa gca      148
Ala Phe Lys Val Arg Leu Ser Ile Arg Thr Ala Leu Gly Asp Lys Ala
10              15              20              25
tat gcc tgg gat acc aat gaa gaa tac ctc ttc aaa gcg atg gta gct      196
Tyr Ala Trp Asp Thr Asn Glu Glu Tyr Leu Phe Lys Ala Met Val Ala
                                30              35              40
ttc tcc atg aga aaa gtt ccc aac aga gaa gca aca gaa att tcc cat      244
Phe Ser Met Arg Lys Val Pro Asn Arg Glu Ala Thr Glu Ile Ser His
                                45              50              55
gtc cta ctt tgc aat gta acc cag agg gta tca ttc tgg ttt gtg gtt      292
Val Leu Leu Cys Asn Val Thr Gln Arg Val Ser Phe Trp Phe Val Val
                                60              65              70
aca gac cct tca aaa aat cac acc ctt cct gct gtt gag gtg caa tca      340
Thr Asp Pro Ser Lys Asn His Thr Leu Pro Ala Val Glu Val Gln Ser
                                75              80              85
gcc ata aga atg aac aag aac cgg atc aac aat gcc ttc ttt cta aat      388
Ala Ile Arg Met Asn Lys Asn Arg Ile Asn Asn Ala Phe Phe Leu Asn
90              95              100              105
gac caa act ctg gaa ttt tta aaa atc cct tcc aca ctt gca cca ccc      436
Asp Gln Thr Leu Glu Phe Leu Lys Ile Pro Ser Thr Leu Ala Pro Pro
                                110              115              120
atg gac cca tct gtg ccc atc tgg att att ata ttt ggt gtg ata ttt      484
Met Asp Pro Ser Val Pro Ile Trp Ile Ile Ile Phe Gly Val Ile Phe
                                125              130              135
tgc atc atc ata gtt gca att gca cta ctg att tta tca ggg atc tgg      532
Cys Ile Ile Ile Val Ala Ile Ala Leu Leu Ile Leu Ser Gly Ile Trp
                                140              145              150
caa cgt ada ara aag aac aaa gaa cca tct gaa gtg gat gac gct gaa      580
Gln Arg Xaa Xaa Lys Asn Lys Glu Pro Ser Glu Val Asp Asp Ala Glu
155              160              165
rat aak tgt gaa aac atg atc aca att gaa aat ggc atc ccc tct gat      628
Xaa Xaa Cys Glu Asn Met Ile Thr Ile Glu Asn Gly Ile Pro Ser Asp
170              175              180              185
ccc ctg gac atg aag gga ggg cat att aat gat gcc ttc atg aca gag      676
Pro Leu Asp Met Lys Gly Gly His Ile Asn Asp Ala Phe Met Thr Glu
                                190              195              200
gat gag agg ctc acc cct ctc tgaagggctg ttgttctgct tcctcaaraa      727
Asp Glu Arg Leu Thr Pro Leu
                                205
attaaacatt tgtttctgtg tgactgctga gcatcctgaa ataccaagag cagatcatat      787
wttttgtttc accattcttc ttttgtaata aattttgaat gtgcttgaaa aaaaaaaaaa      847

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848

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score 10.7
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1 5 10

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25

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ctgccatgta catgatagag agattc

26

<210> 31
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score 0.983
sequence tgtcagttg
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name MYOD_Q6
score 0.961
sequence cccaactgac

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 sequence agataaatcca
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 score 0.958
 sequence cttcagttg
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 name GATA1_02
 score 0.959
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 name TAL1ALPHA47_01
 score 0.973
 sequence cataacagatggtaag
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 score 0.954
 sequence accatctggt
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 score 0.953
 sequence tcaagataaagta
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 score 0.963
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 <221> protein_bind
 <222> 393..404
 <223> matinspector prediction
 name IK2_01
 score 0.985
 sequence agttgggaattc
 <220>
 <221> protein_bind
 <222> 396..405
 <223> matinspector prediction
 name CREL_01
 score 0.962
 sequence tgggaattcc
 <220>
 <221> protein_bind
 <222> 423..436
 <223> matinspector prediction
 name GATA1_02
 score 0.950
 sequence tcagtgatatggca
 <220>
 <221> protein_bind
 <222> complement(478..489)
 <223> matinspector prediction

name SRY_02
 score 0.951
 sequence taaaacaaaaca
 <220>
 <221> protein_bind
 <222> 486..493
 <223> matinspector prediction
 name E2F_02
 score 0.957
 sequence tttagcgc
 <220>
 <221> protein_bind
 <222> complement(514..521)
 <223> matinspector prediction
 name MZF1_01
 score 0.975
 sequence tgagggga
 <400> 31
 tgagtgcagt gttacatgtc agttgggtta agtttggttaa tgtcattcaa atcttctatg 60
 tcttgatttg cctgctaatt ctattatttc tggaactaaa ttagtttgat ggttctatta 120
 gttattgact gaggtgtgct aatctcccat tatgtggatt tatctatttc ttcagttgta 180
 gataggacat tgatagatac ataagtacca ggacaaaagc agggagatct tttttccaaa 240
 atcaggagaa aaaaatgaca tctggaaaac ctatagggaa aggcataaca gatggtaagg 300
 atactttatc ttgagtagga gagccttcct gtggcaacgt ggagaaggga agaggtcgta 360
 gaattgagga gtcagctcag ttagaagcag ggagttggga attccgttca tgtgatttag 420
 catcagtgat atggcaaata tgggactaag ggtagtgatc agagggttaa aattgtgtgt 480
 tttgttttag cgctgctggg gcatcgctt gggtcccctc aaacagattc ccatgaatct 540
 cttcat 546
 <210> 32
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> oligonucleotide
 <400> 32
 gtaccaggga ctgtgaccat tgc 23
 <210> 33
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> oligonucleotide
 <400> 33
 ctgtgaccat tgctcccaag agag 24
 <210> 34
 <211> 861
 <212> DNA
 <213> Homo Sapiens
 <220>
 <221> promoter
 <222> 1..806
 <220>
 <221> transcription start site
 <222> 807
 <220>

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```

<221> protein_bind
<222> complement(60..70)
<223> matinspector prediction
      name NFY_Q6
      score 0.956
      sequence ggaccaatcat
<220>
<221> protein_bind
<222> 70..77
<223> matinspector prediction
      name MZF1_01
      score 0.962
      sequence cctgggga
<220>
<221> protein_bind
<222> 124..132
<223> matinspector prediction
      name CMYB_01
      score 0.994
      sequence tgaccgttg
<220>
<221> protein_bind
<222> complement(126..134)
<223> matinspector prediction
      name VMYB_02
      score 0.985
      sequence tccaacggt
<220>
<221> protein_bind
<222> 135..143
<223> matinspector prediction
      name STAT_01
      score 0.968
      sequence ttcctggaa
<220>
<221> protein_bind
<222> complement(135..143)
<223> matinspector prediction
      name STAT_01
      score 0.951
      sequence ttccaggaa
<220>
<221> protein_bind
<222> complement(252..259)
<223> matinspector prediction
      name MZF1_01
      score 0.956
      sequence ttggggga
<220>
<221> protein_bind
<222> 357..368
<223> matinspector prediction
      name IK2_01
      score 0.965
      sequence gaatgggatttc
<220>
<221> protein_bind
<222> 384..391

```

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<223> matinspector prediction
 name MZF1_01
 score 0.986
 sequence agagggga

<220>

<221> protein_bind
 <222> complement(410..421)

<223> matinspector prediction
 name SRY_02
 score 0.955
 sequence gaaaacaaaaca

<220>

<221> protein_bind
 <222> 592..599

<223> matinspector prediction
 name MZF1_01
 score 0.960
 sequence gaagggga

<220>

<221> protein_bind
 <222> 618..627

<223> matinspector prediction
 name MYOD_Q6
 score 0.981
 sequence agcatctgcc

<220>

<221> protein_bind
 <222> 632..642

<223> matinspector prediction
 name DELTAEF1_01
 score 0.958
 sequence tcccaccttcc

<220>

<221> protein_bind
 <222> complement(813..823)

<223> matinspector prediction
 name S8_01
 score 0.992
 sequence gaggcaattat

<220>

<221> protein_bind
 <222> complement(824..831)

<223> matinspector prediction
 name MZF1_01
 score 0.986
 sequence agagggga

<220>

<221> misc_feature
 <222> 335,376

<223> n=a, g, c or t

<400> 34

tactataggg	cacgcgtggt	cgacggccgg	gctgttctgg	agcagagggc	atgtcagtaa	60
tgattggtcc	ctggggaagg	tctggctggc	tccagcacag	tgaggcattt	aggtatctct	120
cggtgaccgt	tggattcctg	gaagcagtag	ctgttctggt	tggatctggt	agggacaggg	180
ctcagagggc	taggcacgag	ggaaggtcag	aggagaaggs	aggsarggcc	cagtgagarg	240
ggagcatgcc	ttcccccaac	cctggcttsc	ycttggyam	agggcgkttt	tgggmacttr	300
aaytcagggc	ccaascagaa	scacaggccc	aktcntggct	smaagcacia	tagcctgaat	360
gggatttcag	gttagncagg	gtgagagggg	aggctctctg	gcttagtttt	gttttgtttt	420

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ccaaatcaag	gtaacttgct	cccttctgct	acgggccttg	gtcttggtt	gtcctcacc	480
agtcggaact	ccctaccact	ttcaggagag	tggttttagg	cccgtggggc	tgttctgttc	540
caagcagtgt	gagaacatgg	ctggtagagg	ctctagctgt	gtgcggggcc	tgaaggggag	600
tgggttctcg	cccaaagagc	atctgcccc	ttcccacctt	cccttctccc	accagaagct	660
tgcctgagct	gtttggacaa	aaatccaaac	cccacttggc	tactctggcc	tggcttcagc	720
ttggaacca	atacctaggc	ttacaggcca	tcctgagcca	ggggcctctg	gaaattctct	780
tcctgatggt	ccttttaggtt	tgggcacaaa	atataattgc	ctctcccctc	tcccattttc	840
tctcttgga	gcaatggtca	c				861

<210> 35
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> oligonucleotide
 <400> 35
 ctgggatgga aggcacggta

20

<210> 36
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> oligonucleotide
 <400> 36
 gagaccacac agctagacaa

20

<210> 37
 <211> 555
 <212> DNA
 <213> Homo Sapiens
 <220>
 <221> promoter
 <222> 1..500
 <220>
 <221> transcription start site
 <222> 501
 <220>
 <221> protein_bind
 <222> 191..206
 <223> matinspector prediction
 name ARNT_01
 score 0.964
 sequence ggactcacgtgctgct
 <220>
 <221> protein_bind
 <222> 193..204
 <223> matinspector prediction
 name NMYC_01
 score 0.965
 sequence actcacgtgctg
 <220>
 <221> protein_bind
 <222> 193..204
 <223> matinspector prediction
 name USF_01
 score 0.985
 sequence actcacgtgctg

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```

<220>
<221> protein_bind
<222> complement(193..204)
<223> matinspector prediction
      name USF_01
      score 0.985
      sequence cagcacgtgagt
<220>
<221> protein_bind
<222> complement(193..204)
<223> matinspector prediction
      name NMYC_01
      score 0.956
      sequence cagcacgtgagt
<220>
<221> protein_bind
<222> complement(193..204)
<223> matinspector prediction
      name MYCMAX_02
      score 0.972
      sequence cagcacgtgagt
<220>
<221> protein_bind
<222> 195..202
<223> matinspector prediction
      name USF_C
      score 0.997
      sequence tcacgtgc
<220>
<221> protein_bind
<222> complement(195..202)
<223> matinspector prediction
      name USF_C
      score 0.991
      sequence gcacgtga
<220>
<221> protein_bind
<222> complement(210..217)
<223> matinspector prediction
      name MZF1_01
      score 0.968
      sequence catgggga
<220>
<221> protein_bind
<222> 397..410
<223> matinspector prediction
      name ELK1_02
      score 0.963
      sequence ctctccggaagcct
<220>
<221> protein_bind
<222> 400..409
<223> matinspector prediction
      name CETSLP54_01
      score 0.974
      sequence tccggaagcc
<220>
<221> protein_bind

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<222> complement(460..470)
<223> matinspector prediction
      name AP1_Q4
      score 0.963
      sequence agtgactgaac
<220>
<221> protein_bind
<222> complement(460..470)
<223> matinspector prediction
      name AP1FJ_Q2
      score 0.961
      sequence agtgactgaac
<220>
<221> protein_bind
<222> 547..555
<223> matinspector prediction
      name PADS_C
      score 1.000
      sequence tgtggtctc
<400> 37
ctatagggca cgcktggtcg acggcccggg ctggtctggt ctgtkgtgga gtcggggttga      60
aggacagcat ttgtkacatc tgggtctactg caccttcctt ctgccgtgca cttggccttt      120
kawaagctca gcaccggtgc ccatcacagg gccggcagca cacacatccc attactcaga      180
aggaaactgac ggactcacgt gctgctccgt ccccatgagc tcagtggacc tgtctatgta      240
gagcagtcag acagtgcctg ggatagagtg agagttcagc cagtaaatacc aagtgattgt      300
cattcctgtc tgcattagta actcccaacc tagatgtgaa aacttagttc tttctcatag      360
gttgctctgc ccatgggtccc actgcagacc caggcactct ccggaagcct ggaaatcacc      420
cgtgtcttct gcctgctccc gctcacatcc cacacttgtg ttcagtcact gagttacaga      480
ttttgcctcc tcaatttctc ttgtcttagt cccatcctct gttcccctgg ccagtttgtc      540
tagctgtgtg gtctc                                     555

<210> 38
<211> 19
<212> DNA
<213> Artificial Sequence
<220>
<223> oligonucleotide
<400> 38
ggccatacac ttgagtgac                                     19

<210> 39
<211> 19
<212> DNA
<213> Artificial Sequence
<220>
<223> oligonucleotide
<400> 39
atatagacaa acgcacacc                                     19

<210> 40
<211> 1098
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 173..211
<223> Von Heijne matrix
      score 4.19999980926514

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seq MLAVSLTVPLLGA/MM
<220>
<221> polyA_signal
<222> 1063..1068
<220>
<221> polyA_site
<222> 1087..1098
<220>
<221> misc_feature
<222> 144..467
<223> homology
      id :AA057573
      est
<220>
<221> misc_feature
<222> 510..640
<223> homology
      id :AA057573
      est
<220>
<221> misc_feature
<222> 436..523
<223> homology
      id :AA057573
      est
<220>
<221> misc_feature
<222> 708..786
<223> homology
      id :AA057573
      est
<220>
<221> misc_feature
<222> 635..682
<223> homology
      id :AA057573
      est
<220>
<221> misc_feature
<222> 625..1084
<223> homology
      id :N57409
      est
<220>
<221> misc_feature
<222> 779..1084
<223> homology
      id :R71351
      est
<220>
<221> misc_feature
<222> 144..506
<223> homology
      id :H12619
      est
<220>
<221> misc_feature
<222> 90..467

```

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```

<223> homology
      id :T03538
      est
<220>
<221> misc_feature
<222> 314..523
<223> homology
      id :T34150
      est
<220>
<221> misc_feature
<222> 567..687
<223> homology
      id :T34150
      est
<220>
<221> misc_feature
<222> 686..730
<223> homology
      id :T34150
      est
<220>
<221> misc_feature
<222> 510..553
<223> homology
      id :T34150
      est
<220>
<221> misc_feature
<222> 550..579
<223> homology
      id :T34150
      est
<220>
<221> misc_feature
<222> 144..523
<223> homology
      id :N32314
      est
<220>
<221> misc_feature
<222> 510..553
<223> homology
      id :N32314
      est
<220>
<221> misc_feature
<222> 352..523
<223> homology
      id :T77966
      est
<220>
<221> misc_feature
<222> 218..351
<223> homology
      id :T77966
      est
<220>

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... 1944 ...

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<221> misc_feature
<222> 510..553
<223> homology
      id :T77966
      est
<220>
<221> misc_feature
<222> 550..917
<223> homology
      id :AA464128
      est
<220>
<221> misc_feature
<222> 1083
<223> n=a, g, c or t
<400> 40
agtgaggtgg tttctgcggg tgaggctggc gcccgtagca tgagcgaggc ggacgggctg      60
cgacagcgcc ggcccctgcg gcccgcaagt cgtcacagac gatgatggcc aggccccgga      120
ggctaaggac ggcagctcct ttagcggcag agttttccga gtgaccttct tg atg ctg      178
                                   Met Leu
gct gtt tct ctc acc gtt ccc ctg ctt gga gcc atg atg ctg ctg gaa      226
Ala Val Ser Leu Thr Val Pro Leu Leu Gly Ala Met Met Leu Leu Glu
      -10                                -5                                1                                5
tct cct ata gat cca cag cct ctc agc ttc aaa gaa ccc ccg ctc ttg      274
Ser Pro Ile Asp Pro Gln Pro Leu Ser Phe Lys Glu Pro Pro Leu Leu
                                   10                                   15                                   20
ctt ggt gtt ctg cat cca aat acg aag ctg cga cag gca gaa agg ctg      322
Leu Gly Val Leu His Pro Asn Thr Lys Leu Arg Gln Ala Glu Arg Leu
                                   25                                   30                                   35
ttt gaa aat caa ctt gtt gga ccg gag tcc ata gca cat att ggg gat      370
Phe Glu Asn Gln Leu Val Gly Pro Glu Ser Ile Ala His Ile Gly Asp
                                   40                                   45                                   50
gtg atg ttt act ggg aca gca gat ggc cgg gtc gta aaa ctt gaa aat      418
Val Met Phe Thr Gly Thr Ala Asp Gly Arg Val Val Lys Leu Glu Asn
                                   55                                   60                                   65
ggt gaa ata gag acc att gcc cgg ttt ggt tcg ggc cct tgc aaa acc      466
Gly Glu Ile Glu Thr Ile Ala Arg Phe Gly Ser Gly Pro Cys Lys Thr
      70                                   75                                   80                                   85
cga ggt gat gag cct gtg tgt ggg aga ccc ctg ggt atc cgt ggc agg      514
Arg Gly Asp Glu Pro Val Cys Gly Arg Pro Leu Gly Ile Arg Gly Arg
                                   90                                   95                                   100
gcc caa tgg gac tct ctt tgt ggc cga tgc ata caa agg gac tat ttg      562
Ala Gln Trp Asp Ser Leu Cys Gly Arg Cys Ile Gln Arg Asp Tyr Leu
                                   105                                   110                                   115
aag taaatccctg gaaacgtgaa gtgaaactgc tgctgtcctc cgagacaccc      615
Lys
attgagggga agaacatgtc ctttgtgaat gatcttacag tcactcagga tgggaggaag      675
atattatttca ccgattctag cagcaaattg caaagacgag actacctgct tctggtgatg      735
gagggcacag atgacgggag cctgctggag tatgatactg tgaccaggga agtaaaagtt      795
ttattggacc agctgcggtt ccggaatgga gtccagctgt ctccctgcaga agactttgtc      855
ctggtggcag aaacaacat ggccaggata cgaagagtct acgtttcttg cctgatgaag      915
ggcggggctg atctgtttgt ggagaacatg cctggatttc cagacaacat ccggcccagc      975
agctctgggg ggtactgggt gggcatgtcg accatccgcc ctaaccctgg gttttccatg      1035
ctggatttct tatctgagag accctggatt aaaaggatga tttttaangg taaaaaaaaa      1095
aaa                                                                 1098

<210> 41
<211> 855

```



```

<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 267..371
<223> Von Heijne matrix
      score 5.90000009536743
      seq LCGLLHLWLKVFS/LK
<220>
<221> polyA_signal
<222> 817..822
<220>
<221> polyA_site
<222> 842..855
<220>
<221> misc_feature
<222> 608..811
<223> homology
      id :M85769
      est
<400> 41
acaatcagtt tgccaatacc tcagaaacaa atacctcgga caaatctttc tctaaagacc      60
tcagtcagat actagtcaat atcaaatacat gtagatggcg gcatttttagg cctcggacac      120
catccctaca tgacagtgac aatgatgaac tctcctgtag aaaattatat aggagtataa      180
accgaacagg aacagcacaa cctgggaccc agacatgcag tacctctacg caaagtaaaa      240
gtagcagtggt ttcagcacac tttgggt atg ttg act gtt aat gat gta cgt ttc      293
                               Met Leu Thr Val Asn Asp Val Arg Phe
                               -35                               -30
tat aga aat gtc agg tcc aac cat ttc cca ttt gtt cga cta tgt ggt      341
Tyr Arg Asn Val Arg Ser Asn His Phe Pro Phe Val Arg Leu Cys Gly
      -25                               -20                               -15
ctg tta cat tta tgg ctt aaa gtc ttt tct ctt aaa cag tta aaa aaa      389
Leu Leu His Leu Trp Leu Lys Val Phe Ser Leu Lys Gln Leu Lys Lys
      -10                               -5                               1                               5
aaa tct tgg tct aag tat tta ttt gaa tcc tgt tgc tat agg agt ttg      437
Lys Ser Trp Ser Lys Tyr Leu Phe Glu Ser Cys Cys Tyr Arg Ser Leu
      10                               15                               20
tat gtg tgt gtc ttc att taaacatacc tgcatacaaa gatgggtttat      485
Tyr Val Cys Val Phe Ile
      25
ttctatttaa tatgtgacat ttgtttcctg gatatagtcc gtgaaccaca agatttatca      545
tatttttcaa taatatgaga agaaaatggg ccgtaaattg ttaaccattt tatgttcaga      605
tattttctcta gtttttacct agtttgcttt aacatagaga ccagcaagtg aatatatatg      665
cataacctta tatgttgaca caataattca gaataatttg ttaaagataa actaattttt      725
cagagaagaa catttaaagg gttaatatat ttgaaacggt ttcagataat atctatttga      785
ttattgtggc ttctatttga aatgtgtcta aaataaaaatg ctgttttattt aaaatgaaaa      845
aaaaaaaaaa      855

<210> 42
<211> 1176
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 174..266
<223> Von Heijne matrix
      score 3.5
      seq WSPLSTRSGGTHA/CS

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```

<220>
<221> polyA_signal
<222> 1144..1149
<220>
<221> polyA_site
<222> 1165..1176
<220>
<221> misc_feature
<222> 886..1134
<223> homology
      id :AA595193
      est
<220>
<221> misc_feature
<222> 756..894
<223> homology
      id :AA595193
      est
<220>
<221> misc_feature
<222> 655..755
<223> homology
      id :AA595193
      est
<220>
<221> misc_feature
<222> 167..367
<223> homology
      id :W81213
      est
<220>
<221> misc_feature
<222> 66..172
<223> homology
      id :W81213
      est
<220>
<221> misc_feature
<222> 429..508
<223> homology
      id :W81213
      est
<220>
<221> misc_feature
<222> 756..894
<223> homology
      id :AA150887
      est
<220>
<221> misc_feature
<222> 536..643
<223> homology
      id :AA150887
      est
<220>
<221> misc_feature
<222> 655..755
<223> homology

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        id :AA150887
        est
<220>
<221> misc_feature
<222> 429..643
<223> homology
        id :AA493644
        est
<220>
<221> misc_feature
<222> 655..755
<223> homology
        id :AA493644
        est
<220>
<221> misc_feature
<222> 429..643
<223> homology
        id :AA493494
        est
<220>
<221> misc_feature
<222> 655..755
<223> homology
        id :AA493494
        est
<220>
<221> misc_feature
<222> 500..643
<223> homology
        id :AA179182
        est
<220>
<221> misc_feature
<222> 655..755
<223> homology
        id :AA179182
        est
<220>
<221> misc_feature
<222> 756..847
<223> homology
        id :AA179182
        est
<220>
<221> misc_feature
<222> 3..338
<223> homology
        id :HUM524F05B
        est
<220>
<221> misc_feature
<222> 334..374
<223> homology
        id :HUM524F05B
        est
<220>
<221> misc_feature

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```

<222> 886..1134
<223> homology
      id :AA398156
      est
<220>
<221> misc_feature
<222> 756..894
<223> homology
      id :AA398156
      est
<220>
<221> misc_feature
<222> 590,601
<223> n=a, g, c or t
<400> 42
aaaaacaata ggacggaaac gccgaggaac ccggctgagg cggcagagca tcctggccag      60
aacaagccaa ggagccaaga cgagagggac acacggacaa acaacagaca gaagacgtac      120
tggccgctgg actccgctgc ctcccccatc tccccgccat ctgcgcccgg agg atg      176
                                     Met
agc cca gcc ttc agg gcc atg gat gtg gag ccc cgc gcc aaa ggc tcc      224
Ser Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly Ser
-30                               -25                               -20                               -15
ttc tgg agc cct ttg tcc acc agg tcg ggg ggc act cat gcg tgc tcc      272
Phe Trp Ser Pro Leu Ser Thr Arg Ser Gly Gly Thr His Ala Cys Ser
                               -10                               -5                               1
gct tca atg aga caa ccc tgg gca agc ccc tgg tcc caa ggg aac atc      320
Ala Ser Met Arg Gln Pro Trp Ala Ser Pro Trp Ser Gln Gly Asn Ile
                               5                               10                               15
agt tct acg aga ccc tcc ctg ctg aga tgc gca aat tct ctc ccc agt      368
Ser Ser Thr Arg Pro Ser Leu Leu Arg Cys Ala Asn Ser Leu Pro Ser
                               20                               25                               30
aca aag gac aaa gcc aaa ggc ccc ttg tta gct ggc cat ccc tgc ccc      416
Thr Lys Asp Lys Ala Lys Gly Pro Leu Leu Ala Gly His Pro Cys Pro
35                               40                               45                               50
att ttt tcc cct ggt cct ttc ccc tgt ggc cac agg gaa gtg tgg cct      464
Ile Phe Ser Pro Gly Pro Phe Pro Cys Gly His Arg Glu Val Trp Pro
                               55                               60                               65
gaa tac ccc acc ccg gct cct ctg cac cca gag ctg ggg gcc acc tca      512
Glu Tyr Pro Thr Pro Ala Pro Leu His Pro Glu Leu Gly Ala Thr Ser
                               70                               75                               80
gaa gtg tca tct ctc tct gag cac gsa ttc ccc tgc agc agt cga gga      560
Glu Val Ser Ser Leu Ser Glu His Xaa Phe Pro Cys Ser Ser Arg Gly
                               85                               90                               95
ctg agc aga ttg agt gat gct ggg gca gan adg cct gag ang aaa ggt      608
Leu Ser Arg Leu Ser Asp Ala Gly Ala Xaa Xaa Pro Glu Xaa Lys Gly
100                               105                               110
gtt cag cca gtc gtt tgt aag gcg ctc gkc ggm act gct gaa acg ccc      656
Val Gln Pro Val Val Cys Lys Ala Leu Xaa Gly Thr Ala Glu Thr Pro
115                               120                               125                               130
cca ccc tgacagcccc atcctcaaag actgtcttaa ttactcatgg caggttctag      712
Pro Pro
agacttaagg ggaaaagctg ctttcaaggc caccacatgt ctggtgctcc ccmaccagst      772
statctgcct wgtgttcatt ttgytatatt gtgasgtgag acagcaaaga ccaataaaaa      832
catattttat aagaacaaaa ggcytgggtg cctaccgkg tgggggcacw gtgggaagcc      892
ttctgmtagg gtgtcttgtg ctgtrtgggt tgttttgttt gccccyttat tttgctttgc      952
ttaccagtc ttcccytamt yttggatgst tyttaaccct caggcaaacc tgtgttcccc      1012
ctgtattcag gstygtcttt aaagcaagcc atgaggctgt tggagtttct gtttagggca      1072
ttaaaaattc ccgcaaacta taaagagcaa tgttttcagt yttttaggat tagaagaatt      1132

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acataaaaat taataaacat tttcaatgat ggaaaaaaa aaaa

1176

<210> 43
<211> 648
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 460..555
<223> Von Heijne matrix
score 4
seq FSFMLLGMMGGCLP/GF

<220>
<221> polyA_signal
<222> 614..619
<220>
<221> polyA_site
<222> 635..648

<400> 43
aattctggcc cagcttcttc cccagctcta tcctgcttcc ctccatctcc tataggattc 60
tccttagagt tctccctcca ttagtagttg tcttaggggc tggttctggg gagccctgcc 120
taagactcat gctacaagaa gttaaataag tttcccgaag tcacacagct agcctctcat 180
cccttttcta ctgagaggaa gtggaatgca ctccgacaag gataagggtt tattgtgagc 240
tggccttgga attaaaccac caccaacaca cttttggatt atcagaagggt ggaaggagtg 300
caaatgccag ttacgggtgat gcgttcaaca tccttatttc cagtctttat gacgcctttc 360
ctgaatcaca ggtgcattgg ggtgcttctt cctccccagg actcccaccc aactttgtga 420
acacaacca cttagaggag ttatctcagc acattatga atg ttg ggg acc acg 474

Met Leu Gly Thr Thr

-30

ggc ctc ggg aca cag ggt cct tcc cag cag gct ctg ggc ttt ttc tcc 522
Gly Leu Gly Thr Gln Gly Pro Ser Gln Gln Ala Leu Gly Phe Phe Ser
-25 -20 -15

ttt atg tta ctt gga atg ggc ggg tgc ctg cct gga ttc ctg cta cag 570
Phe Met Leu Leu Gly Met Gly Gly Cys Leu Pro Gly Phe Leu Leu Gln
-10 -5 1 5

cct ccc aat cga tct cct act ttg cct gca tcc acc ttt gcc cat 615
Pro Pro Asn Arg Ser Pro Thr Leu Pro Ala Ser Thr Phe Ala His
10 15 20

taaagtcaat tctccacca taaaaaaaaaaa aaa 648

<210> 44
<211> 1251
<212> DNA
<213> Homo sapiens
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<221> sig_peptide
<222> 79..369
<223> Von Heijne matrix
score 4
seq RLPLVVSFIASSS/AN

<220>
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<222> 1217..1222
<220>
<221> polyA_site
<222> 1240..1251
<220>
<221> misc_feature


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<222> 2..423
<223> homology
      id :AA056667
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<220>
<221> misc_feature
<222> 463..520
<223> homology
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      est
<220>
<221> misc_feature
<222> 418..467
<223> homology
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<220>
<221> misc_feature
<222> 159..636
<223> homology
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<220>
<221> misc_feature
<222> 629..684
<223> homology
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      est
<220>
<221> misc_feature
<222> 5..453
<223> homology
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<220>
<221> misc_feature
<222> 446..494
<223> homology
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<220>
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<222> 14..343
<223> homology
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<220>
<221> misc_feature
<222> 323..467
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<220>
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<222> 463..494
<223> homology
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      est

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157


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<222> 14..475
<223> homology
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<220>
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<222> 410..876
<223> homology
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      est

<220>
<221> misc_feature
<222> 974..1195
<223> homology
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      est

<220>
<221> misc_feature
<222> 769..982
<223> homology
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      est

<220>
<221> misc_feature
<222> 1208..1237
<223> homology
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      est

<220>
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<222> 223..522
<223> homology
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<220>
<221> misc_feature
<222> 518..636
<223> homology
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      est

<220>
<221> misc_feature
<222> 774..1127
<223> homology
      id :N94607
      est

<220>
<221> misc_feature
<222> 690..765
<223> homology
      id :N94607
      est

<220>
<221> misc_feature
<222> 833..1195
<223> homology

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102

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id :AA076410
est
<400> 44
aaagtgacag cggagagaac caggsagccc agaaacccca ggcgtggaga ttgattcctgc      60
gagagaaggg ggttcattc atg gcg gat gac cta aag cga ttc ttg tat aaa      111
                Met Ala Asp Asp Leu Lys Arg Phe Leu Tyr Lys
                -95                -90
aag tta cca agt gtt gaa ggg ctc cat gcc att gtt gtg tca gat aga      159
Lys Leu Pro Ser Val Glu Gly Leu His Ala Ile Val Val Ser Asp Arg
-85                -80                -75
gat gga gta cct gtt att aaa gtg gca aat gac aat gct cca gag cat      207
Asp Gly Val Pro Val Ile Lys Val Ala Asn Asp Asn Ala Pro Glu His
-70                -65                -60                -55
gct ttg cga cct ggt ttc tta tcc act ttt gcc ctt gca aca gac caa      255
Ala Leu Arg Pro Gly Phe Leu Ser Thr Phe Ala Leu Ala Thr Asp Gln
                -50                -45                -40
gga agc aaa ctt gga ctt tcc aaa aat aaa agt atc atc tgt tac tat      303
Gly Ser Lys Leu Gly Leu Ser Lys Asn Lys Ser Ile Ile Cys Tyr Tyr
-35                -30                -25
aac acc tac cag gtg gtt caa ttt aat cgt tta cct ttg gtg gtg agt      351
Asn Thr Tyr Gln Val Val Gln Phe Asn Arg Leu Pro Leu Val Val Ser
-20                -15                -10
ttc ata gcc agc agc agt gcc aat aca gga cta att gtc agc cta gaa      399
Phe Ile Ala Ser Ser Ser Ala Asn Thr Gly Leu Ile Val Ser Leu Glu
-5                1                5                10
aag gag ctt gct cca ttg ttt gaa gaa ctg aga caa gtt gtg gaa att      447
Lys Glu Leu Ala Pro Leu Phe Glu Glu Leu Arg Gln Val Val Glu Ile
                15                20                25
tct taatctgaca gtggtttcag tgtgtacctt atcttcatta taacaacaca      500
Ser
atatcaatcc agcaatcttt agactacaat aatgctttta tccatgtgct caagaaaggg      560
cccccttttc caacttatac taaagaacta gcatatagat gtaatttata gatagatcag      620
ttgctatatt ttctgggtgta aggtctttct tatttagtga gatctaggga taccacagaa      680
atggttcagt ctatcacagc tcccatggag ttagtctggt caccagatat ggatgagaga      740
ttctattcag tggattagaa tcaaactggt acattgatcc acttgagccg ttaagtgtg      800
ccaattgtac aatatgcccga ggcttgcaga ataaagccaa cttttttattg tgaataataa      860
taaggacata tttttcttca gattatgttt tatttctttg cattgagtga ggtacataaa      920
atggcttggt aaaagtaata aaatcagtag aatcactaac tttcctttgt acatattatt      980
ttgcagtata gatgaatatt actaatcagt ttgattattc tcagagggtg ctgctcttta      1040
atgaaaatga aaattatagc taatgttttt tcctcaaact ctgctttctg taaccaatca      1100
gtgtttttaat gtttgtgtgt tcttcataaa atttaaatac aattcgttat tctgtttcca      1160
atgttagtat gtatgtaaac atgatagtag agccattttt ttcatatgtg agtaaaaata      1220
aaatagtatt tttaaaagta aaaaaaaaaa a      1251

<210> 45
<211> 1524
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 160..231
<223> Von Heijne matrix
        score 5.69999980926514
        seq ILGLLGLLGLTLVA/ML
<220>
<221> polyA_signal
<222> 1510..1515
<220>

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159


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<221> polyA_site
<222> 1506..1519
<220>
<221> misc_feature
<222> 1048..1504
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<220>
<221> misc_feature
<222> 597..846
<223> homology
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<220>
<221> misc_feature
<222> 39..93
<223> homology
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      est
<220>
<221> misc_feature
<222> 113..149
<223> homology
      id :AA345449
      est
<220>
<221> misc_feature
<222> 98..400
<223> homology
      id :T86266
      est
<220>
<221> misc_feature
<222> 1210..1489
<223> homology
      id :T86158
      est
<220>
<221> misc_feature
<222> 954..983
<223> homology
      id :AA116709
      est
<400> 45
agctgcttgt ggccacccac agacacttgt aaggaggaga gaagtcagcc tggcagagag      60
actctgaaat gassgattag aggtgttcaa ggragcaaag agcttcagcc tgaagacaag      120
ggagcagtcc ctgaagacgc ttctactgag aggtctgcc atg gcc tct ctt ggc      174
                                   Met Ala Ser Leu Gly
                                   -20
ctc caa ctt gtg ggc tac atc cta ggc ctt ctg ggg ctt ttg ggc aca      222
Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu Leu Gly Leu Leu Gly Thr
                                   -15                                   -10                                   -5
ctg gtt gcc atg ctg ctc ccc agc tgg aaa aca agt tct tat gtc ggt      270
Leu Val Ala Met Leu Leu Pro Ser Trp Lys Thr Ser Ser Tyr Val Gly
                                   1                                   5                                   10
gcc agc att gtg aca gca gtt ggc ttc tcc aag ggc ctc tgg atg gaa      318
Ala Ser Ile Val Thr Ala Val Gly Phe Ser Lys Gly Leu Trp Met Glu

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168



15	20	25	
tgt gcc aca cac agc aca ggc atc acc cag tgt gac atc tat agc acc			366
Cys Ala Thr His Ser Thr Gly Ile Thr Gln Cys Asp Ile Tyr Ser Thr			
30	35	40	45
ctt ctg ggc ctg ccc gct gac atc cak gct gcc cag gcc atg atg gtg			414
Leu Leu Gly Leu Pro Ala Asp Ile Xaa Ala Gln Ala Met Met Val			
50	55	60	
aca tcc agt gca atc tcc tcc ctg gcc tgc att atc tct gtg gtg ggc			462
Thr Ser Ser Ala Ile Ser Ser Leu Ala Cys Ile Ile Ser Val Val Gly			
65	70	75	
atg ara tgc aca gtc ttc tgc cag gaa tcc cga gcc aaa gac aga gtg			510
Met Xaa Cys Thr Val Phe Cys Gln Glu Ser Arg Ala Lys Asp Arg Val			
80	85	90	
gcg gta gca ggt gga gtc ttt ttc atc ctt gga ggc ctc ctg gga ttc			558
Ala Val Ala Gly Gly Val Phe Phe Ile Leu Gly Gly Leu Leu Gly Phe			
95	100	105	
att cct gtt gcc tgg aat ctt cat ggg atc cta cgg gac ttc tac tca			606
Ile Pro Val Ala Trp Asn Leu His Gly Ile Leu Arg Asp Phe Tyr Ser			
110	115	120	125
cca ctg gtg cct gac agc atg aaa ttt gag att gga gag gct ctt tac			654
Pro Leu Val Pro Asp Ser Met Lys Phe Glu Ile Gly Glu Ala Leu Tyr			
130	135	140	
ttg ggc att att tct tcc ctg ttc tcc ctg ata gct gga atc atc ctc			702
Leu Gly Ile Ile Ser Ser Leu Phe Ser Leu Ile Ala Gly Ile Ile Leu			
145	150	155	
tgc ttt tcc tgc tca tcc cag aga aat cgc tcc aac tac tac gat gcc			750
Cys Phe Ser Cys Ser Ser Gln Arg Asn Arg Ser Asn Tyr Tyr Asp Ala			
160	165	170	
tac caa gcc caa cct ctt gcc aca agg agc tct cca agg cct ggt caa			798
Tyr Gln Ala Gln Pro Leu Ala Thr Arg Ser Ser Pro Arg Pro Gly Gln			
175	180	185	
cct ccc aaa gtc aag agt gag ttc aat tcc tac agc ctg aca ggg tat			846
Pro Pro Lys Val Lys Ser Glu Phe Asn Ser Tyr Ser Leu Thr Gly Tyr			
190	195	200	205
gtg tgaagaacca ggggccagag ctgggggggtg gctgggtctg tgaaaaaacag			899
Val			
tggacagcac cccgagggcc acaggtgagg gacactacca ctggatcgtg tcagaaggtg			959
ctgctgaggg tagactgact ttggccattg gattgagcaa aggcagaaat gggggctagt			1019
gtaacagcat gcaggttgaa ttgccaagga tgctcgccat gccagccttt ctgttttcct			1079
caccttgctg ctcccctgcc ctaagtcccc aaccctcaac ttgaaacccc attcccttaa			1139
gccaggamtc agaggatccc tytgccctck ggtttamctg ggactccatc cccaaaccca			1199
ctaatacacat cccactgact gaccctctgt gatcaaagac cctccctctg gctgaggttg			1259
gstyttagct cattgctggg gatgggaagg agaagcagtg gctttysttg gcattgctyt			1319
aacctamtty tcaagcttcc ctccaaagaa amtgattggc cctggaacct ccatccact			1379
yttgttatga ctccacagtg tccagamtaa tttgtgcatg aactgaaata aaaccatcct			1439
acggtatyca gggaacagaa agcaggatgc aggatgggag gacaggaagg cagcctggga			1499
catttaaaaa aataaaaaaa aaaaa			1524

<210> 46
 <211> 610
 <212> DNA
 <213> Homo sapiens
 <220>
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 <222> 106..201
 <223> Von Heijne matrix
 score 8.80000019073486
 seq VPMLLLIVGGSFG/LR

161


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<220>
<221> polyA_signal
<222> 577..582
<220>
<221> polyA_site
<222> 598..610
<220>
<221> misc_feature
<222> 68..167
<223> homology
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<220>
<221> misc_feature
<222> 166..262
<223> homology
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<220>
<221> misc_feature
<222> 423..520
<223> homology
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      est
<220>
<221> misc_feature
<222> 518..564
<223> homology
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<221> misc_feature
<222> 276..313
<223> homology
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<223> homology
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<221> misc_feature
<222> 41..262
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<222> 423..520
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<220>
<221> misc_feature
<222> 518..564
<223> homology

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<220>
<221> misc_feature
<222> 276..313
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<220>
<221> misc_feature
<222> 46..262
<223> homology
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<220>
<221> misc_feature
<222> 2..39
<223> homology
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<220>
<221> misc_feature
<222> 455..493
<223> homology
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<220>
<221> misc_feature
<222> 276..313
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<220>
<221> misc_feature
<222> 423..458
<223> homology
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<220>
<221> misc_feature
<222> 53..262
<223> homology
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        est
<220>
<221> misc_feature
<222> 423..520
<223> homology
        id :AA044291
        est
<220>
<221> misc_feature
<222> 518..564
<223> homology
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        est
<220>
<221> misc_feature

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163


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<222> 276..313
<223> homology
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<220>
<221> misc_feature
<222> 125..262
<223> homology
      id :W47031
      est
<400> 46
aaagtgagtt aaggacgtac tcgtcttggt gagagcgtga stgctgagat ttgggagttct      60
gcgctaggcc cgcttgaggt tctgagccga tggaagagtt cactc atg ttt gca ccc      117
                                         Met Phe Ala Pro
                                         -30
gcg gtg atg cgt gct ttt cgc aag aac aag act ctc ggc tat gga gtc      165
Ala Val Met Arg Ala Phe Arg Lys Asn Lys Thr Leu Gly Tyr Gly Val
                    -25                    -20                    -15
ccc atg ttg ttg ctg att gtt gga ggt tct ttt ggt ctt cgt gag ttt      213
Pro Met Leu Leu Leu Ile Val Gly Gly Ser Phe Gly Leu Arg Glu Phe
                    -10                    -5                    1
tct caa atc cga tat gat gct gtg aag agt aaa atg gat cct gag ctt      261
Ser Gln Ile Arg Tyr Asp Ala Val Lys Ser Lys Met Asp Pro Glu Leu
5                    10                    15                    20
gaa aaa aaa ccg aaa gag aat aaa ata tct tta gag tcg gaa tat gag      309
Glu Lys Lys Pro Lys Glu Asn Lys Ile Ser Leu Glu Ser Glu Tyr Glu
                    25                    30                    35
gga agt atc tgt tgaagggcta ctatctttcc ttggcccttc tcccttggtg      361
Gly Ser Ile Cys
                    40
ggactcaatc tccagactat ctccccagag aatcttgtca aggcttggct ttaagctttg      421
ttgggaaaat caaagactcc aagtttgatg actggaagaa tattcgagga cccaggcctt      481
gggaagatcc tgacctctc caaggaagaa atccaggaaa gccttaagac taagacaact      541
tgactctgct gattcttttt tccttttttt ttttaaataa aaatactatt aactggaaaa      601
aaaaaaaaa      610

<210> 47
<211> 1370
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 359..466
<223> Von Heijne matrix
      score 7.80000019073486
      seq LTFLFLHLPPSTS/LF
<220>
<221> polyA_signal
<222> 1334..1339
<220>
<221> polyA_site
<222> 1357..1370
<220>
<221> misc_feature
<222> 113..420
<223> homology
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      est

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164


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<220>
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<222> 406..482
<223> homology
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<220>
<221> misc_feature
<222> 199..420
<223> homology
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<220>
<221> misc_feature
<222> 406..514
<223> homology
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<220>
<221> misc_feature
<222> 2..269
<223> homology
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      est

<220>
<221> misc_feature
<222> 406..646
<223> homology
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      est

<220>
<221> misc_feature
<222> 647..682
<223> homology
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      est

<220>
<221> misc_feature
<222> 439..646
<223> homology
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      est

<220>
<221> misc_feature
<222> 647..739
<223> homology
      id :AA450228
      est

<220>
<221> misc_feature
<222> 406..646
<223> homology
      id :R02473
      est

<220>
<221> misc_feature
<222> 406..604
<223> homology

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165


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        id :T71107
        est
<220>
<221> misc_feature
<222> 71..282
<223> homology
        id :C06030
        est
<220>
<221> misc_feature
<222> 319..365
<223> homology
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        est
<220>
<221> misc_feature
<222> 2..57
<223> homology
        id :C06030
        est
<220>
<221> misc_feature
<222> 1173..1277
<223> homology
        id :N54909
        est
<220>
<221> misc_feature
<222> 1080..1177
<223> homology
        id :N54909
        est
<220>
<221> misc_feature
<222> 1273..1356
<223> homology
        id :N54909
        est
<220>
<221> misc_feature
<222> 1173..1277
<223> homology
        id :AA196824
        est
<220>
<221> misc_feature
<222> 1080..1177
<223> homology
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<220>
<221> misc_feature
<222> 1273..1356
<223> homology
        id :AA196824
        est

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<400> 47
acaaggcaga gcttctgaat ttcaggcctt cattccagag ccctcttggtg gccaggcctt

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60

166



cctttgctgg	aggaaggtac	acaggggtgaa	gctgawgstg	tacttggggg	atctccttgg	120
cctgttccac	caagtgagag	aaggtactta	ctcttgtacc	tcctgttcag	ccaggtgcat	180
taacagacct	ccctacagct	gtaggaacta	ctgtcccaga	gctgaggcaa	ggggatttct	240
caggtcattt	ggagaacaag	tgcttttagta	gtagttttaa	gtagtaactg	ctactgtatt	300
tagtgggggtg	gaattcagaa	gaaatttgaa	gaccagatca	tgggtggtct	gcatgtga	358
atg aac ach	ttt gag cca	gac agc ctg	gct gtc att	gct ttc ttc	ctc	406
Met Asn Thr	Phe Glu Pro	Asp Ser Leu	Ala Val Ile	Ala Phe Phe	Leu	
-35		-30		-25		
ccc att tgg	acc ttc tct	gcc ctt aca	ttt ttg ttt	ctc cat cta	cca	454
Pro Ile Trp	Thr Phe Ser	Ala Leu Thr	Phe Leu Phe	Leu His Leu	Pro	
-20		-15		-10	-5	
cca tcc acc	agt cta ttt	att aac tta	gca aga gga	caa ata aag	ggc	502
Pro Ser Thr	Ser Leu Phe	Ile Asn Leu	Ala Arg Gly	Gln Ile Lys	Gly	
	1	5		10		
cct ctt ggc	ttg att ttg	ctt ctt tct	ttc tgt gga	gga tat act	aag	550
Pro Leu Gly	Leu Ile Leu	Leu Leu Ser	Phe Cys Gly	Gly Tyr Thr	Lys	
	15	20		25		
tgc gac ttt	gcc cta tcc	tat ttg gaa	atc cct aac	aga att gag	ttt	598
Cys Asp Phe	Ala Leu Ser	Tyr Leu Glu	Ile Pro Asn	Arg Ile Glu	Phe	
30		35		40		
tct att atg	gat cca aaa	aga aaa aca	aaa tgc taatgaagcc	atcasgtcaa		651
Ser Ile Met	Asp Pro Lys	Arg Lys Thr	Lys Cys			
45		50		55		
gggtcacatg	ccaataaaca	ataaattttc	cagaagaaat	gaaatccaac	tagacaaata	711
aagtagagct	tatgaaatgg	ttcagtaagg	atgagcttgt	tgttttttgt	tttgttttgt	771
tttgtttttt	taaagacgga	gtctcgctct	gtcactcagg	ctggagtgca	gtggtatgat	831
cttggtcac	tgtaacctcc	gcctcccggg	ttcaagccat	tctcctgcct	cagtctcctg	891
agtagctggg	attgcaggtg	cgtgccacca	tgcttggtta	atttttgtgt	ttttggtaga	951
gacaggggtt	caccacgttg	gtcgggctgg	tctcgggctc	ctgacctctt	gatccgcctg	1011
ccttggcctc	ccaaagtgat	gggattacag	atgtgagcca	ccgtgcctag	ccaaggatga	1071
gattttttaa	gtatgttcca	gttctgtgtc	atgggttgaa	gacagagtag	gaaggatatg	1131
gaaaagggtc	tggggaagca	gaggtgattc	atggctctgt	ggaatttgag	gtgaatgggt	1191
ccttattgtc	taggccactt	gtgaagaata	tgagtcagtt	attgccagcc	ttggaattta	1251
cttctctagc	ttacaatgga	cctttttgaa	ctgggaaaca	ccttgtctgc	attcacttta	1311
aaatgtcaaa	actaattttt	ataataaatg	tttattttca	catygaaaaa	aaaaaaaaa	1370

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<211> 791

<212> DNA

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<222> 191..286

<223> Von Heijne matrix

score 8.80000019073486

seq VPMLLLIVGGSFG/LR

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<221> polyA_signal

<222> 755..760

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<221> polyA_site

<222> 780..791

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<221> misc_feature

<222> 361..531

<223> homology

id :W73841

est

167


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<222> 361..530
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      est

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<222> 361..531
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        id :AA531561
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169


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gagcaccaaa taaccaagga aaaggaagtg agttaaggac gtactcgtct tggtagagagc      120
gtgagctgct gagatttggg agtctgcgct aggcccgtt ggagttctga gccgatggaa      180
gagttcactc atg ttt gca ccc gcg gtg atg cgt gct ttt cgc aag aac      229
          Met Phe Ala Pro Ala Val Met Arg Ala Phe Arg Lys Asn
                -30                -25                -20
aag act ctc ggc tat gga gtc ccc atg ttg ttg ctg att gtt gga ggt      277
Lys Thr Leu Gly Tyr Gly Val Pro Met Leu Leu Leu Ile Val Gly Gly
                -15                -10                -5
tct ttt ggt ctt cgt gag ttt tct caa atc cga tat gat gct gtg aag      325
Ser Phe Gly Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp Ala Val Lys
                1                5                10
ggt aaa atg gat cct gag ctt gaa aaa aaa ctg aaa gag aat aaa ata      373
Gly Lys Met Asp Pro Glu Leu Glu Lys Lys Leu Lys Glu Asn Lys Ile
                15                20                25
tct tta gag tcg gaa tat gag aaa atc aaa gac tcc aag ttt gat gac      421
Ser Leu Glu Ser Glu Tyr Glu Lys Ile Lys Asp Ser Lys Phe Asp Asp
30                35                40                45
tgg aag aat att cga gga ccc agg cct tgg gaa gat cct gac ctc ctc      469
Trp Lys Asn Ile Arg Gly Pro Arg Pro Trp Glu Asp Pro Asp Leu Leu
                50                55                60
caa gga aga aat cca gaa agc ctt aag act aag aca act tgactctgct      518
Gln Gly Arg Asn Pro Glu Ser Leu Lys Thr Lys Thr Thr
                65                70
gattctcttt tccttttttt ttttaaataa aaatactatt aactggactt cctaatatat      578
acttctatca agtggaaagg aaattccagg cccatggaaa cttggatatg ggtaatttgg      638
atggacaaaa ktaatctkct actaaaggct atgtaccagg tttttatact tcccagctaa      698
ttccatctgt ggatgaaagt tgcaatgttg gcccccgat katttttacac cntcgaaata      758
aaaaatgtga ataactgctc caaaaaaaaaaaa aaa      791

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<210> 49
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<213> Homo sapiens
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<223> Von Heijne matrix
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      seq SFLPSALVIWTS/AF
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<221> polyA_signal
<222> 1400..1405
<220>
<221> polyA_site
<222> 1420..1433
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<221> misc_feature
<222> 268..634
<223> homology
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<220>
<221> misc_feature
<222> 118..564

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170


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<223> homology
      id :N27248
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<220>
<221> misc_feature
<222> 268..697
<223> homology
      id :N44490
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<220>
<221> misc_feature
<222> 582..687
<223> homology
      id :AA274731
      est
<220>
<221> misc_feature
<222> 65..369
<223> homology
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<220>
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<222> 471..519
<223> homology
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<222> 61..399
<223> homology
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<223> homology
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<222> 484..699
<223> homology
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      est
<220>
<221> misc_feature
<222> 685..772
<223> homology
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      est
<220>
<221> misc_feature
<222> 454..486
<223> homology
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      est
<220>

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<223> homology
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      est
<220>
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<222> 572..687
<223> homology
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      est
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<221> misc_feature
<222> 260..444
<223> homology
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      est
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<221> misc_feature
<222> 449..567
<223> homology
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      est
<220>
<221> misc_feature
<222> 117..184
<223> homology
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      est
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<221> misc_feature
<222> 260..464
<223> homology
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      est
<220>
<221> misc_feature
<222> 118..184
<223> homology
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<222> 56..113
<223> homology
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<220>
<221> misc_feature
<222> 454..485
<223> homology
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      est
<220>
<221> misc_feature
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<223> n=a, g, c or t
<400> 49

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1000

1000

1000

actcctttta	gcataggggc	ttcggcgcca	gcgccagcg	ctagtcggtc	tggtaagtgc	60
ctgatgccga	gttccgtctc	tcgcgtcttt	tcctgggtccc	aggcaaagcg	gasgnagatc	120
ctcaaacggc	ctagtgttcc	gcgcttccgg	agaaaatcag	cgggtctaatt	aattcctctg	180
gtttgttgaa	gcagttacca	agaatcttca	accctttccc	acaaaagcta	attgagtaca	240
cgttcctggt	gagtacacgt	tcctgttgat	ttacaaaagg	tgcaggtatg	agcaggtctg	300
aagactaaca	ttttgtgaag	ttgtaaaaca	gaaaacctgt	tagaa atg	tgg tgg ttt	357
				Met Trp Trp Phe		

-20

cag	caa	ggc	ctc	agt	ttc	ctt	cct	tca	gcc	ctt	gta	att	tgg	aca	tct	405
Gln	Gln	Gly	Leu	Ser	Phe	Leu	Pro	Ser	Ala	Leu	Val	Ile	Trp	Thr	Ser	

-15

-10

-5

gct	gct	ttc	ata	ttt	tca	tac	att	act	gca	gta	aca	ctc	cac	cat	ata	453
Ala	Ala	Phe	Ile	Phe	Ser	Tyr	Ile	Thr	Ala	Val	Thr	Leu	His	His	Ile	

1

5

10

15

gac	ccg	gct	tta	cct	tat	atc	agt	gac	act	ggc	aca	gta	gct	cca	gaa	501
Asp	Pro	Ala	Leu	Pro	Tyr	Ile	Ser	Asp	Thr	Gly	Thr	Val	Ala	Pro	Glu	

20

25

30

aaa	tgc	tta	ttt	ggg	gca	atg	cta	aat	att	gcg	gca	ggt	tta	tgc	att	549
Lys	Cys	Leu	Phe	Gly	Ala	Met	Leu	Asn	Ile	Ala	Ala	Val	Leu	Cys	Ile	

35

40

45

gct	acc	att	tat	gtt	cgt	tat	aag	caa	gtt	cat	gct	ctg	agt	cct	gaa	597
Ala	Thr	Ile	Tyr	Val	Arg	Tyr	Lys	Gln	Val	His	Ala	Leu	Ser	Pro	Glu	

50

55

60

gag	aac	gtt	atc	atc	aaa	tta	aac	aag	gct	ggc	ctt	gta	ctt	gga	ata	645
Glu	Asn	Val	Ile	Ile	Lys	Leu	Asn	Lys	Ala	Gly	Leu	Val	Leu	Gly	Ile	

65

70

75

ctg	agt	tgt	tta	gga	ctt	tct	att	gtg	gca	aac	ttc	cag	gaa	aac	aac	693
Leu	Ser	Cys	Leu	Gly	Leu	Ser	Ile	Val	Ala	Asn	Phe	Gln	Glu	Asn	Asn	

80

85

90

95

cct	ttt	tgc	tgc	aca	tgt	aag	tgg	agc	tgt	gct	tac	ctt	tgg	tat	ggg	741
Pro	Phe	Cys	Cys	Thr	Cys	Lys	Trp	Ser	Cys	Ala	Tyr	Leu	Trp	Tyr	Gly	

100

105

110

ctc	att	ata	tat	gtt	tgt	tca	gac	cat	cct	ttc	cta	cca	aaa	tgc	agc	789
Leu	Ile	Ile	Tyr	Val	Cys	Ser	Asp	His	Pro	Phe	Leu	Pro	Lys	Cys	Ser	

115

120

125

cca	aaa	tcc	aat	ggc	aaa	aca	agt	ctt	ctg	gat	cag	act	ggt	ggt	ggg	837
Pro	Lys	Ser	Asn	Gly	Lys	Thr	Ser	Leu	Leu	Asp	Gln	Thr	Val	Val	Gly	

130

135

140

tat	ctg	gtg	tgg	agt	aag	tgc	act	tagcatgctg	acttgctcat	cagttttgca	891
Tyr	Leu	Val	Trp	Ser	Lys	Cys	Thr				

145

150

cagtggcaat	tttgggactg	atttagaaca	gaaactccat	tggaaaccccg	aggacaaagg	951
ttatgcgctt	cacatgatca	ctactgcagc	agaatgggtct	atgtcattttt	ccttcttttg	1011
ttttttcctg	acttacattc	gtgattttca	gaaaattttcc	ttacgggtgg	aagccaactt	1071
acatggatta	accctctatg	acactgcacc	ttgccctatt	aacaatgaac	gaacacggct	1131
actttccags	aagatattag	atgaaaggat	aaaatatttc	tgtaantgan	ttastgastt	1191
ctcagggant	tggggaaang	gttcacagaa	gttgcttavt	tcttcacrt	gaanattttc	1251
aanccactta	antcaaggct	gacagstaac	acgtgatgaa	tgctgataat	caggaaacat	1311
gaaagaagcc	atttgcatag	attattytaa	aggatatcat	caagaagamt	attaaaaaca	1371
cctatgccta	tactttttta	tytcagaaaa	taaagtcaaa	agactatgaa	aaaaaaaaaa	1431
aa						1433

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<211> 1158

<212> DNA

<213> Homo sapiens

<220>

<221> sig_peptide

173


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<222> 214..339
<223> Von Heijne matrix
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<221> polyA_signal
<222> 1133..1138
<220>
<221> polyA_site
<222> 1146..1158
<220>
<221> misc_feature
<222> 840..968
<223> homology
      id :H64717
      est
<220>
<221> misc_feature
<222> 858..968
<223> homology
      id :H65208
      est
<220>
<221> misc_feature
<222> 652
<223> n=a, g, c or t
<400> 50
aarttgagct tggggactgc agctgtgggg agatttcagt gcattgcctc ccctgggtgc      60
tcttcatctt ggatttgaaa gttgagagca gcatgttttg cccactgaaa ctcacccctgs    120
tgrsagtgta mtggattatt ccttgggcct gaatgacttg aatgtttccc cgcctgagct    180
aacagtcctat gtgggtgatt cagctctgat ggg atg tgt ttt cca gag cac aga     234
                               Met Cys Phe Pro Glu His Arg
                               -40
aga caa atg tat att caa gat aga ctg gac tct gtc acc agg aga gca      282
Arg Gln Met Tyr Ile Gln Asp Arg Leu Asp Ser Val Thr Arg Arg Ala
-35                               -30                               -25                               -20
cgc caa gga cga ata tgt gct ata cta tta ctc caa tct cag tgt gcc      330
Arg Gln Gly Arg Ile Cys Ala Ile Leu Leu Leu Gln Ser Gln Cys Ala
                               -15                               -10                               -5
tat tgg gcg ctt cca gaa ccg cgt aca ctt gat ggg gga cat ctt atg      378
Tyr Trp Ala Leu Pro Glu Pro Arg Thr Leu Asp Gly Gly His Leu Met
                               1                               5                               10
caa tgatggctct ctccctgctcc aagatgtgca agaggctgac cagggaacct      431
Gln
atatctgtga aatccgcctc aaagggggaga gccaggtggt caagaaggcg gtgggtactgc    491
atgtgcttcc agaggagccc aaaggtacgc aaatgcttac ttaaagaggg gccaaggggc    551
aagagctttc atgtgcaaga ggcaaggaaa ctgattatct tgagtaaagt ccagcctttg    611
ggctaagtac ttaccacaga gtgaatcttc aaagaaatga ntcattaaat tatttcagrt    671
cagaataaaa atakgagtta ttttagttaa kaataaaaata ttgataatta ttgtattatt    731
actttaaaaca cacttcccc ctcacaaaagc cctgtgaagg atgttttggt cacatataat    791
gtccaaatat gttttggaca catatattatt aaatggaata aatagtamtt gaaccctggc    851
accthtgaca acaaagtcya tgattytttt actatgccct aataccttts atcagttatc    911
cacattgatg ctacatytgt attttatagg taccctatgt taggtgtttt gggggataga    971
aaagaaataa gcagkycagg ctcaagtggct catgcctgta atcctagcat tttgggaggc   1031
tgaggcagca gaamtgcctg agccccaggg ttcaagactg cagtgaagcta tgawggcacc   1091
actgcattyt agcctgggwg acagagcaag actygtgtta aaataaaaaa agagaaaaaa   1151
aaaaaaa                                           1158

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174


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<212> DNA
<213> Homo sapiens
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<223> Von Heijne matrix
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<222> 812..817
<220>
<221> polyA_site
<222> 838..850
<220>
<221> misc_feature
<222> 128..424
<223> homology
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<221> misc_feature
<222> 61..128
<223> homology
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<220>
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<222> 483..554
<223> homology
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<222> 417..464
<223> homology
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<222> 460..500
<223> homology
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<222> 577..612
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<222> 612..649
<223> homology
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175


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<223> homology
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<222> 128..294
<223> homology
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<221> misc_feature
<222> 370..509
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<220>
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<222> 505..591
<223> homology
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<220>
<221> misc_feature
<222> 293..330
<223> homology
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<220>
<221> misc_feature
<222> 22..57
<223> homology
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<220>
<221> misc_feature
<222> 95..128
<223> homology
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<220>
<221> misc_feature
<222> 128..326
<223> homology
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      est
<220>
<221> misc_feature
<222> 418..605
<223> homology

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176


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id :AA186399
est
<220>
<221> misc_feature
<222> 326..423
<223> homology
id :AA186399
est
<220>
<221> misc_feature
<222> 39..128
<223> homology
id :AA186399
est
<220>
<221> misc_feature
<222> 206..640
<223> homology
id :W52489
est
<400> 51
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accatggcgt atcacggcct cactgtgcct ctcattgtga tgagcgtggt ctggggcttc 120
gtcggccttc ttgggtgcctt gggtcatccc taagggtcct aaccggggag ttatcattac 180
catgttggtg acctgttcag tttgctgcta tctcttttgg ctgattgcaa ttctggccca 240
actcaaccct ctctttggac cgcaattgaa aaatgaaacc atctgggtatc tgaagtatca 300
ttggccttga ggaagaagac atgctctaca gtgctcagtc tttgaggtca cgagaagaga 360
atgccttcta g atg caa aat cac ctc caa acc aga cca ctt ttc ttg act 410
Met Gln Asn His Leu Gln Thr Arg Pro Leu Phe Leu Thr
-20 -15 -10
tgc ctg ttt tgg cca tta gct gcc tta aac gtt aac agc aca ttt gaa 458
Cys Leu Phe Trp Pro Leu Ala Ala Leu Asn Val Asn Ser Thr Phe Glu
-5 1 5
tgc ctt att cta caa tgc agc gtg ttt tcc ttt gcc ttt ttt gca ctt 506
Cys Leu Ile Leu Gln Cys Ser Val Phe Ser Phe Ala Phe Phe Ala Leu
10 15 20
tgg tgaattacgt gcctccataa cctgaactgt gccgactcca caaaacgatt 559
Trp
atgtactctt ctgagataga agatgctggt cttctgagag atacgttact ctctccttgg 619
aatctgtgga tttgaaaatg gctcctgcct tctcacgtgg gaatcagtga agtggtttaga 679
aactgctgca agacaaacaa gactccagtg ggggtggtcag taggaaaaca cgttcagagg 739
gaagaaccat ctcaacagaa tcgcaccaaa ctatactttc aggatgaatt tcttctttct 799
gccatctttt ggaataaata ttttcctcct ttytatgtaa aaaaaaaaaa a 850

<210> 52
<211> 1107
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 132..215
<223> Von Heijne matrix
score 3.59999990463257
seq PLSDSWALLPASA/GV
<220>
<221> polyA_signal
<222> 1069..1074
<220>

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177


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<221> polyA_site
<222> 1094..1107
<220>
<221> misc_feature
<222> 177..392
<223> homology
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<220>
<221> misc_feature
<222> 425..542
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<220>
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<222> 43..114
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<222> 551..590
<223> homology
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<220>
<221> misc_feature
<222> 166..314
<223> homology
      id :AA043154
      est
<220>
<221> misc_feature
<222> 27..181
<223> homology
      id :AA043154
      est
<220>
<221> misc_feature
<222> 425..564
<223> homology
      id :AA043154
      est
<220>
<221> misc_feature

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<222> 387..441
<223> homology
      id :AA043154
      est
<220>
<221> misc_feature
<222> 309..352
<223> homology
      id :AA043154
      est
<220>
<221> misc_feature
<222> 549..580
<223> homology
      id :AA043154
      est
<220>
<221> misc_feature
<222> 601..1071
<223> homology
      id :AA126732
      est
<220>
<221> misc_feature
<222> 576..605
<223> homology
      id :AA126732
      est
<220>
<221> misc_feature
<222> 387..477
<223> homology
      id :AA161280
      est
<220>
<221> misc_feature
<222> 292..362
<223> homology
      id :AA161280
      est
<220>
<221> misc_feature
<222> 46..113
<223> homology
      id :AA161280
      est
<220>
<221> misc_feature
<222> 217..277
<223> homology
      id :AA161280
      est
<220>
<221> misc_feature
<222> 113..160
<223> homology
      id :AA161280
      est

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<220>
<221> misc_feature
<222> 173..217
<223> homology
      id :AA161280
      est
<400> 52
aacaacttcc ggccccactg agcgggtgtcc tgagccgatt acagctaggt agtggagcgc      60
cgctgcttac ctgggtgcag gagacagccg gagtcgctgg gggagctccg cgccgccgga      120
cgcccgtgac c atg tgg agg ctg ctg gct cgc gct agt gcg ccg ctc ctg      170
      Met Trp Arg Leu Leu Ala Arg Ala Ser Ala Pro Leu Leu
              -25                      -20

cgg gtg ccc ttg tca gat tcc tgg gca ctc ctc ccc gcc agt gct ggc      218
Arg Val Pro Leu Ser Asp Ser Trp Ala Leu Leu Pro Ala Ser Ala Gly
-15                      -10                      -5                      1
gta aag aca ctg ctc cca gta cca agt ttt gaa gat gtt tcc att cct      266
Val Lys Thr Leu Leu Pro Val Pro Ser Phe Glu Asp Val Ser Ile Pro
              5                      10                      15

gaa aaa ccc aag ctt aga ttt att gaa agg gca cca ctt gtg cca aaa      314
Glu Lys Pro Lys Leu Arg Phe Ile Glu Arg Ala Pro Leu Val Pro Lys
              20                      25                      30

gta aga aga gaa cct aaa aat tta agt gac ata cgg gga cct tcc act      362
Val Arg Arg Glu Pro Lys Asn Leu Ser Asp Ile Arg Gly Pro Ser Thr
              35                      40                      45

gaa gct acg gag kkk aca gaa ggc aat ttt gca atc ttg gca ttg ggt      410
Glu Ala Thr Glu Xaa Thr Glu Gly Asn Phe Ala Ile Leu Ala Leu Gly
50                      55                      60                      65

ggg ggc tac ctg cat tgg ggc cac ttt gaa atg atg cgc ctg aca atc      458
Gly Gly Tyr Leu His Trp Gly His Phe Glu Met Met Arg Leu Thr Ile
              70                      75                      80

aac cgc tct atg gac ccc aag aac atg ttt gcc ata tgg cga gta cca      506
Asn Arg Ser Met Asp Pro Lys Asn Met Phe Ala Ile Trp Arg Val Pro
              85                      90                      95

gcc cct ttc aag ccc atc act cgc aaa agt gtt ggg cat cgc atg ggg      554
Ala Pro Phe Lys Pro Ile Thr Arg Lys Ser Val Gly His Arg Met Gly
              100                      105                      110

gga ggc aaa ggt gct att gac cac tac gtg aca cct gtg aag gct ggc      602
Gly Gly Lys Gly Ala Ile Asp His Tyr Val Thr Pro Val Lys Ala Gly
              115                      120                      125

cgc mww gww gta gag atg ggt ggg cgt tgt gma ttt gaa gaa gtg caa      650
Arg Xaa Xaa Val Glu Met Gly Gly Arg Cys Xaa Phe Glu Glu Val Gln
130                      135                      140                      145

ggg ttc ctt gac cag gtt gcc cac aag ttg ccc tty gca gca aag gct      698
Gly Phe Leu Asp Gln Val Ala His Lys Leu Pro Phe Ala Ala Lys Ala
              150                      155                      160

gtg agc cgc ggg act yta gag aag atg cga aaa gat caa gag gaa aga      746
Val Ser Arg Gly Thr Leu Glu Lys Met Arg Lys Asp Gln Glu Glu Arg
              165                      170                      175

gaa mgt aac aac cag aac ccc tgg aca ttt gag cga ata gcc act gcc      794
Glu Xaa Asn Asn Gln Asn Pro Trp Thr Phe Glu Arg Ile Ala Thr Ala
              180                      185                      190

mac atg ctg ggc ata cgg aaa gta ctg agc cca tat gac ttg acc cac      842
Xaa Met Leu Gly Ile Arg Lys Val Leu Ser Pro Tyr Asp Leu Thr His
              195                      200                      205

aag ggg aaa tam tgg ggc aag tty tac atg ccc mam cgt gtg      884
Lys Gly Lys Xaa Trp Gly Lys Phe Tyr Met Pro Xaa Arg Val
210                      215                      220

tagtgagtgt aggagataac tgtatatagg stactgaaag aaggattytg catttytatt      944

```

180

cccctcagcc tacccactga agtytttggg tagctyttaa gccataamta aggagcagca	1004
tttgagtaga tttytgaaaa acgatgttat ttgttgattt aaaaagaaaa cwgtattttt	1064
attaaataaa atttaaacad cacttcagga aaaaaaaaaa aaa	1107

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<210> 53
<211> 500
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 199..288
<223> Von Heijne matrix
      score 5.59999990463257
      seq IVSVLALIPETTT/LT
<220>
<221> polyA_signal
<222> 464..469
<220>
<221> polyA_site
<222> 489..500
<220>
<221> misc_feature
<222> 197..412
<223> homology
      id :AA429945
      est
<220>
<221> misc_feature
<222> 61..195
<223> homology
      id :AA429945
      est
<220>
<221> misc_feature
<222> 425..488
<223> homology
      id :AA429945
      est
<220>
<221> misc_feature
<222> 197..412
<223> homology
      id :AA455042
      est
<220>
<221> misc_feature
<222> 61..195
<223> homology
      id :AA455042
      est
<220>
<221> misc_feature
<222> 425..488
<223> homology
      id :AA455042
      est
<220>
<221> misc_feature

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<222> 207..412
<223> homology
      id :W93646
      est
<220>
<221> misc_feature
<222> 58..195
<223> homology
      id :W93646
      est
<220>
<221> misc_feature
<222> 425..488
<223> homology
      id :W93646
      est
<220>
<221> misc_feature
<222> 197..412
<223> homology
      id :AA516431
      est
<220>
<221> misc_feature
<222> 90..195
<223> homology
      id :AA516431
      est
<220>
<221> misc_feature
<222> 425..488
<223> homology
      id :AA516431
      est
<220>
<221> misc_feature
<222> 52..195
<223> homology
      id :W38899
      est
<220>
<221> misc_feature
<222> 197..324
<223> homology
      id :W38899
      est
<220>
<221> misc_feature
<222> 443..477
<223> homology
      id :W38899
      est
<220>
<221> misc_feature
<222> 197..338
<223> homology
      id :W52820
      est

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<220>
<221> misc_feature
<222> 71..195
<223> homology
      id :W52820
      est
<220>
<221> misc_feature
<222> 339..401
<223> homology
      id :W52820
      est
<220>
<221> misc_feature
<222> 425..469
<223> homology
      id :W52820
      est
<220>
<221> misc_feature
<222> 40..195
<223> homology
      id :W19506
      est
<220>
<221> misc_feature
<222> 9..10,12
<223> n=a, g, c or t
<400> 53
agagctgtnn cnsaagtagg ggagggcggt gctccgcmgm ggtggcggdh tgctatcgct      60
tcgcagaacc tactcaggca gccagctgag aagagttgag ggaaagtgct gctgctgggt      120
ctgcagacgc gatggataac gtgcagccga aaataaaaca tcgccccttc tgcttcagtg      180
tgaaggcca cgtgayag atg ctg cgg ctg gat att atc aac tca ctg gta      231
                Met Leu Arg Leu Asp Ile Ile Asn Ser Leu Val
                -30                -25                -20
aca aca gta ttc atg ctc atc gta tct gtg ttg gca ctg ata cca gaa      279
Thr Thr Val Phe Met Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu
                -15                -10                -5
acc aca aca ttg aca gtt ggt gga ggg gtg ttt gca ctt gtg aca gca      327
Thr Thr Thr Leu Thr Val Gly Gly Gly Val Phe Ala Leu Val Thr Ala
                1                5                10
gta tgc tgt ctt gcc gac ggg gcc ctt att tac cgg aag ctt ctg ttc      375
Val Cys Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe
                15                20                25
aat ccc agc ggt cct tac cag aaa aag cct gtg cat gaa aaa aaa gaa      423
Asn Pro Ser Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu
                30                35                40                45
gtt ttg taattttata ttacttttta gtttgatact aagtattaaa catatttctg      479
Val Leu
tattcttcca aaaaaaaaaa a      500

<210> 54
<211> 765
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 293..385

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<223> Von Heijne matrix
      score 4.40000009536743
      seq TCCHLGLPHPVRA/PR
<220>
<221> polyA_signal
<222> 733..738
<220>
<221> polyA_site
<222> 752..765
<220>
<221> misc_feature
<222> 310..576
<223> homology
      id :HUM426A07B
      est
<220>
<221> misc_feature
<222> 119
<223> n=a, g, c or t
<400> 54
aaaccttggt gctagggacc gggcgggttg cggcaaccgt gggcactgct gaatttgaat      60
tgagggggcga gggaaaagtt ttcctcaggt gtggtgggga gagggaggcg gatgccggng      120
aaaccgtagg kacgcggtca gaaaggcgac gggctgtcgg agttggaaag ggacgcctgg      180
tttcccccca agcgaaccgg gatgggaagt gacttcaatg agattgaact tcagctggat      240
tgaaagagag gctagaagtt ccgcttgcca gcagcctcct tagtagagcg ga atg agt      298
                                         Met Ser
                                         -30

aat acc cac acg gtg ctt gtc tca ctt ccc cat ccg cac ccg gcc ctc      346
Asn Thr His Thr Val Leu Val Ser Leu Pro His Pro His Pro Ala Leu
                        -25                        -20                        -15

acc tgc tgt cac ctc ggc ctc cca cac ccg gtc cgc gct ccc cgc cct      394
Thr Cys Cys His Leu Gly Leu Pro His Pro Val Arg Ala Pro Arg Pro
                        -10                        -5                        1

ctt cct cgc gta gaa ccg tgg gat cct agg tgg cag gac tca gag cta      442
Leu Pro Arg Val Glu Pro Trp Asp Pro Arg Trp Gln Asp Ser Glu Leu
      5                        10                        15

agg tat cca cag gcc atg aat tcc ttc cta aat gag cgg tca tcg ccg      490
Arg Tyr Pro Gln Ala Met Asn Ser Phe Leu Asn Glu Arg Ser Ser Pro
      20                        25                        30                        35

tgc agg acc tta agg caa gaa gca tcg gct gac aga tgt gat ctc      535
Cys Arg Thr Leu Arg Gln Glu Ala Ser Ala Asp Arg Cys Asp Leu
                        40                        45                        50

tgaacctgat agattgctga ttttatctta ttttatcctt gacttggtac aagttttggg      595
atttctgaaa agaccataca gataaccaca aatatcaaga aagtcgtctt cagtattaag      655
tagaatttag atttaggttt ccttcctgct tcccacctcc ttcgaataag gaaacgtctt      715
tgggaccaac tttatggaat aaataagctg agctgcaaaa waaaaaaaaa      765

<210> 55
<211> 584
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 130..189
<223> Von Heijne matrix
      score 3.5
      seq KFCLICLLTFIFH/HC
<220>

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<221> polyA_signal
<222> 546..551
<220>
<221> polyA_site
<222> 572..584
<400> 55
aagacgcgcc ggtttctgcg acgcagtttag cgcagtctgc tttggtgaat acacgatttg      60
gtgcagccgg ggtttggtac cgagcggaga ggagatgcac acggcactcg agtgtgagga      120
aaaatagaa atg aag gta cat atg cac aca aaa ttt tgc ctc att tgt ttg      171
      Met Lys Val His Met His Thr Lys Phe Cys Leu Ile Cys Leu
      -20                      -15                      -10
ctg aca ttt att ttt cat cat tgc aac cat tgc cat gaa gaa cat gac      219
Leu Thr Phe Ile Phe His His Cys Asn His Cys His Glu Glu His Asp
      -5                      1                      5                      10
cat ggc cct gaa gcg ctt cac aga cag cat cgt gga atg aca gaa ttg      267
His Gly Pro Glu Ala Leu His Arg Gln His Arg Gly Met Thr Glu Leu
      15                      20                      25
gag cca agc aaa ttt tca aag caa gct gct gaa aat gaa aaa aaa tac      315
Glu Pro Ser Lys Phe Ser Lys Gln Ala Ala Glu Asn Glu Lys Lys Tyr
      30                      35                      40
tat att gaa aaa ctt ttt gag cgt tat ggt gaa aat gga aga tta tcc      363
Tyr Ile Glu Lys Leu Phe Glu Arg Tyr Gly Glu Asn Gly Arg Leu Ser
      45                      50                      55
ttt ttt ggt ttg gag aaa ctt tta aca aac ttg ggc ctt gga gag aga      411
Phe Phe Gly Leu Glu Lys Leu Leu Thr Asn Leu Gly Leu Gly Glu Arg
      60                      65                      70
aaa gta gtt gag att aat cat gag gat ctt ggc cac gat cat gtt tct      459
Lys Val Val Glu Ile Asn His Glu Asp Leu Gly His Asp His Val Ser
      75                      80                      85                      90
cat tta agg tat ttt ggc agt tca aga ggg aaa gca ttt tca ctc aca      507
His Leu Arg Tyr Phe Gly Ser Ser Arg Gly Lys Ala Phe Ser Leu Thr
      95                      100                      105
taaccaccca gcattcccat aatcatttaa attcagaaaa tcaaaactgt gaccagtgtgta      567
wtccacaaaa aaaaaaa      584

```

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<210> 56
<211> 1387
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 191..325
<223> Von Heijne matrix
      score 4.59999990463257
      seq VLVYLVTAERVWS/DD
<220>
<221> polyA_signal
<222> 1348..1353
<220>
<221> polyA_site
<222> 1374..1387
<220>
<221> misc_feature
<222> 1258..1372
<223> homology
      id :AA417826
      est
<220>

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<221> misc_feature
<222> 791..887
<223> homology
      id :AA417826
      est
<220>
<221> misc_feature
<222> 94..524
<223> homology
      id :AA235826
      est
<220>
<221> misc_feature
<222> 44..94
<223> homology
      id :AA235826
      est
<220>
<221> misc_feature
<222> 1258..1372
<223> homology
      id :AA236941
      est
<220>
<221> misc_feature
<222> 935..1279
<223> homology
      id :AA480326
      est
<220>
<221> misc_feature
<222> 1258..1372
<223> homology
      id :AA480326
      est
<220>
<221> misc_feature
<222> 724..1148
<223> homology
      id :AA234245
      est
<220>
<221> misc_feature
<222> 944..1279
<223> homology
      id :AA479344
      est
<220>
<221> misc_feature
<222> 1258..1372
<223> homology
      id :AA479344
      est
<220>
<221> misc_feature
<222> 1070..1212
<223> homology
      id :AA133636

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```

      est
<220>
<221> misc_feature
<222> 1258..1372
<223> homology
      id :AA133636
      est
<220>
<221> misc_feature
<222> 938..1054
<223> homology
      id :AA133636
      est
<220>
<221> misc_feature
<222> 94..436
<223> homology
      id :AA133635
      est
<220>
<221> misc_feature
<222> 32..94
<223> homology
      id :AA133635
      est
<220>
<221> misc_feature
<222> 895..1273
<223> homology
      id :AA479453
      est
<220>
<221> misc_feature
<222> 1258..1371
<223> homology
      id :AA253214
      est
<220>
<221> misc_feature
<222> 94..268
<223> homology
      id :AA482378
      est
<220>
<221> misc_feature
<222> 946
<223> n=a, g, c or t
<400> 56
actcccaggc tgggccagca caccggcag gctctgtcct ggaaacaggc ttcaacgggc      60
ttccccgaaa accttccccg cttctggata tgaavattca agctgcttgc tgagtcctat      120
tgccggctgc tgggagccag gagagccctg aggagtagtc actcagtagc agctgacgcg      180
tgggtccacc atg aac tgg agt atc ttt gag gga ctc ctg agt ggg gtc      229
          Met Asn Trp Ser Ile Phe Glu Gly Leu Leu Ser Gly Val
          -45                -40                -35
aac aag tac tcc aca gcc ttt ggg cgc atc tgg ctg tct ctg gtc ttc      277
Asn Lys Tyr Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe
          -30                -25                -20
atc ttc cgc gtg ctg gtg tac ctg gtg acg gcc gag cgt gtg tgg agt      325

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Ile	Phe	Arg	Val	Leu	Val	Tyr	Leu	Val	Thr	Ala	Glu	Arg	Val	Trp	Ser		
-15						-10					-5						
gat	gac	cac	aag	gac	ttc	gac	tgc	aat	act	cgc	cag	ccc	ggc	tgc	tcc	373	
Asp	Asp	His	Lys	Asp	Phe	Asp	Cys	Asn	Thr	Arg	Gln	Pro	Gly	Cys	Ser		
1			5					10					15				
aac	gtc	tgc	ttt	gat	gag	ttc	ttc	cct	gtg	tcc	cat	gtg	cgc	ctc	tgg	421	
Asn	Val	Cys	Phe	Asp	Glu	Phe	Phe	Pro	Val	Ser	His	Val	Arg	Leu	Trp		
			20					25					30				
gcc	ctg	cag	ctt	atc	ctg	gtg	aca	tgc	ccc	tca	ctg	ctc	gtg	gtc	atg	469	
Ala	Leu	Gln	Leu	Ile	Leu	Val	Thr	Cys	Pro	Ser	Leu	Leu	Val	Val	Met		
			35				40					45					
cac	gtg	gcc	tac	cgg	gag	gtt	cag	gag	aag	agg	cac	cga	gaa	gcc	cat	517	
His	Val	Ala	Tyr	Arg	Glu	Val	Gln	Glu	Lys	Arg	His	Arg	Glu	Ala	His		
			50			55					60						
ggg	gag	aac	agt	ggg	cgc	ctc	tac	ctg	aac	ccc	ggc	aag	aar	cgg	ggt	565	
Gly	Glu	Asn	Ser	Gly	Arg	Leu	Tyr	Leu	Asn	Pro	Gly	Lys	Lys	Arg	Gly		
65					70				75					80			
ggg	ctc	tgg	tgg	aca	tat	gtc	tgc	agc	cta	gtg	ttc	aag	gcg	agc	gtg	613	
Gly	Leu	Trp	Trp	Thr	Tyr	Val	Cys	Ser	Leu	Val	Phe	Lys	Ala	Ser	Val		
				85				90					95				
gac	atc	gcc	ttt	ctc	tat	gtg	ttc	cac	tca	ttc	tac	ccc	aaa	tat	atc	661	
Asp	Ile	Ala	Phe	Leu	Tyr	Val	Phe	His	Ser	Phe	Tyr	Pro	Lys	Tyr	Ile		
			100					105					110				
ctc	cct	cct	gtg	gtc	aag	tgc	cac	gca	gat	cca	tgt	ccc	aat	ata	gtg	709	
Leu	Pro	Pro	Val	Val	Lys	Cys	His	Ala	Asp	Pro	Cys	Pro	Asn	Ile	Val		
			115				120					125					
gac	tgc	ttc	atc	tcc	aag	ccc	tca	gag	aag	aac	att	ttc	acc	ctc	ttc	757	
Asp	Cys	Phe	Ile	Ser	Lys	Pro	Ser	Glu	Lys	Asn	Ile	Phe	Thr	Leu	Phe		
			130			135					140						
atg	gtg	gcc	aca	gct	gcc	atc	tgc	atc	ctg	ctc	aac	ctc	gtg	gag	ctc	805	
Met	Val	Ala	Thr	Ala	Ala	Ile	Cys	Ile	Leu	Leu	Asn	Leu	Val	Glu	Leu		
				145		150			155				160				
atc	tac	ctg	gtg	agc	aag	aga	tgc	cac	gag	tgc	ctg	gca	gca	agg	aaa	853	
Ile	Tyr	Leu	Val	Ser	Lys	Arg	Cys	His	Glu	Cys	Leu	Ala	Ala	Arg	Lys		
				165				170					175				
gct	caa	gcc	atg	kgc	aca	ggt	cat	cac	ccc	cav	gat	acc	acy	ttt	tcc	901	
Ala	Gln	Ala	Met	Xaa	Thr	Gly	His	His	Pro	Xaa	Asp	Thr	Thr	Phe	Ser		
			180				185						190				
kgc	aaa	caa	gas	gac	ytic	ytt	tcg	gk	gac	ytic	atc	ttt	ctg	ggn	tca	949	
Xaa	Lys	Gln	Xaa	Asp	Xaa	Xaa	Ser	Gly	Asp	Xaa	Ile	Phe	Leu	Gly	Ser		
			195				200					205					
gac	agt	cat	cyt	cct	ytic	tta	cca	gac	cgc	ccc	cga	gac	cat	gtg	aag	997	
Asp	Ser	His	Xaa	Pro	Xaa	Leu	Pro	Asp	Arg	Pro	Arg	Asp	His	Val	Lys		
			210			215					220						
aaa	acc	aty	ttg	tgaggggctg	cctggamtgg	tytggcaggt	tgggcctgga									1049	
Lys	Thr	Ile	Leu														
225																	
tgaggaggct	ytagcatyty	tcataggtgc	aacctgagag	tgaggaggct	aagccatgag											1109	
gtaggggag	gcaagagaga	ggattcagac	gytytgggag	ccagttccta	gtcctcaamt											1169	
ccagccacct	gccccagsth	gacggcamtg	ggccagttcc	ccctytgsty	tgcagstcgg											1229	
tttctttty	tagaatggaa	atagtggagg	ccaatgccca	gggttgagg	gaggagggcg											1289	
ttcatagaag	aacacacatg	cgggcacctt	catygtgtgt	ggcccactgt	cagaacttaa											1349	
taaaagtcaa	mtcatttgct	ggttaaaaaa	aaaaaaaa													1387	

<210> 57
 <211> 1385
 <212> DNA
 <213> Homo sapiens


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<220>
<221> sig_peptide
<222> 141..251
<223> Von Heijne matrix
      score 4
      seq PLSLDCGHSLCRA/CI
<220>
<221> polyA_signal
<222> 1354..1359
<220>
<221> polyA_site
<222> 1375..1385
<220>
<221> misc_feature
<222> 1183..1240
<223> homology
      id :AA463623
      est
<220>
<221> misc_feature
<222> 176..239
<223> homology
      id :AA258927
      est
<220>
<221> misc_feature
<222> 803..854
<223> homology
      id :AA286417
      est
<220>
<221> misc_feature
<222> 1183..1213
<223> homology
      id :AA608077
      est
<400> 57
aacacccacc ctggcttttc ttcacctctt caaccaggag ccgagatttc tggtgctctg      60
aagccatcca ggggtcttta accagaagag agaggagagc ctcaggagtt aggaccagaa      120
gaagccaggg aagcagtgca atg gct tca aaa atc ttg ctt aac gta caa gag      173
                               Met Ala Ser Lys Ile Leu Leu Asn Val Gln Glu
                               -35                               -30

gag gtg acc tgt ccc atc tgc ctg gag ctg ttg aca gaa ccc ttg agt      221
Glu Val Thr Cys Pro Ile Cys Leu Glu Leu Leu Thr Glu Pro Leu Ser
      -25                               -20                               -15

cta gac tgt ggc cac agc ctc tgc cga gcc tgc atc act gtg agc aac      269
Leu Asp Cys Gly His Ser Leu Cys Arg Ala Cys Ile Thr Val Ser Asn
      -10                               -5                               1                               5

aag gag gca gtg acc agc atg gga gga aaa agc agc tgt cct gtg tgt      317
Lys Glu Ala Val Thr Ser Met Gly Gly Lys Ser Ser Cys Pro Val Cys
                               10                               15                               20

ggt atc agt tac tca ttt gaa cat cta cag gct aat cag cat cgg gcc      365
Gly Ile Ser Tyr Ser Phe Glu His Leu Gln Ala Asn Gln His Arg Ala
                               25                               30                               35

aac ata gtg gag aga ctc aag gag gtc aag ttg agc cca gac aat ggg      413
Asn Ile Val Glu Arg Leu Lys Glu Val Lys Leu Ser Pro Asp Asn Gly
                               40                               45                               50

aag aag aga gat ctc tgt gat cat cat gga gag aaa ctc cta ctc ttc      461

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189

Lys	Lys	Arg	Asp	Leu	Cys	Asp	His	His	Gly	Glu	Lys	Leu	Leu	Leu	Phe	
55					60					65					70	
tgt	aag	gag	gat	agg	aaa	gtc	att	tgc	tgg	ctt	tgt	gag	cgg	tct	cag	509
Cys	Lys	Glu	Asp	Arg	Lys	Val	Ile	Cys	Trp	Leu	Cys	Glu	Arg	Ser	Gln	
				75				80						85		
gag	cac	cgt	ggt	cac	cac	aca	ggt	cct	cac	gga	gga	agt	att	caa	gga	557
Glu	His	Arg	Gly	His	His	Thr	Gly	Pro	His	Gly	Gly	Ser	Ile	Gln	Gly	
			90					95					100			
atg	tca	gga	gaa	act	cca	ggc	agt	cct	caa	gag	gct	gaa	gaa	gga	aga	605
Met	Ser	Gly	Glu	Thr	Pro	Gly	Ser	Pro	Gln	Glu	Ala	Glu	Glu	Gly	Arg	
		105					110					115				
gga	gga	agc	tgagaagctg	gaagctgaca	tcagagaaga	gaaaacttcc										654
Gly	Gly	Ser														
		120														
tggaagtatc	aggtacaaac	tgagagacaa	aggatacaaa	cagaatttga	tcagctttaga											714
agcatcctaa	ataatgagga	gcagagagag	ctgcaaagat	tggaagaaga	agaaaagaag											774
acgctggata	agtttgcaga	ggctgaggat	gagctagttc	agcagaagca	gttggtgaga											834
gagctcatct	cagatgtgga	gtgtcggagt	cagtgggtcaa	caatggagct	gctgcaggac											894
atgagtggaa	tcatgaaatg	gagtggagtc	tggaggctga	aaaagccaaa	aatggtttcc											954
aagaaactga	agactgtatt	ccatgctcca	gatctgagta	ggatgctgcr	aatgttttaga											1014
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tgggaagtgg	acgtgtccaa	gaaaactgcc	tggatcctgg	gggtatactg	tagaacatat											1254
tcccgccata	tgaagtatgt	tgttagaaga	tgtgcaaaty	gtcaaaatbt	ttacaccaaa											1314
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aaaaaaaaa	a															1385

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 <222> 958..1110
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 est
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190


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agactgggtg cctgggagct gaggcagcca ccgtttcagc ctggccagcc ctctggaccc      180
cgaggttgga ccctactgtg acacacctac c atg cgg aca ctc ttc aac ctc      232
Met Arg Thr Leu Phe Asn Leu

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192

[illegible][illegible]

-15

ctc tgg ctt gcc ctg gcc tgc agc cct* gtt cac act acc ctg tca aag	280
Leu Trp Leu Ala Leu Ala Cys Ser Pro Val His Thr Thr Leu Ser Lys	
-10 -5 1	
tca gat gcc asa aaa ccg cct caa aga cgc tgc tgg aga aga gtc agt	328
Ser Asp Ala Xaa Lys Pro Pro Gln Arg Arg Cys Trp Arg Arg Val Ser	
5 10 15 20	
ttt cag ata agc cgg tgc aar acc ggg gtt tgg tgg tgacggacct	374
Phe Gln Ile Ser Arg Cys Lys Thr Gly Val Trp Trp	
25 30	
caaagctgag agtgtgggttc ttgagcatcg cagctactgc tcggcaaagg cccgggacag	434
acacttttgct ggggatgtac tgggctatgt cactccatgg aacagccatg gctacgatgt	494
caccaaggtc tttgggagca agttcacaca gatctcacc gtctggctgc agttgaagag	554
acgtggccgt gagatgtttg aggtcacggg cctccacgac gtggaccaag ggtggatgcg	614
agctgtcagg aagcatgcca agggcctgca catagtgcct cggctcctgt ttgaggactg	674
gacttacgat gatttccgga acgtcttaga cagtgaggat gagatagagg agctgagcaa	734
gaccgtggtc caggtggcaa agaaccagca tttcgatggc ttcgtgggtg aggtctggaa	794
ccagctgcta agccagaagc gcgtgggcct catccacatg ctcacccact tggccgaggc	854
cctgcaccag gcccggtgc tggccctcct ggatcatcccg cctgccatca cccccgggac	914
cgaccagctg ggcattgtca cgcacaagga gtttgagcag ctggcccccg tgctggatgg	974
tttcagcctc atgacctacg actactctac agcgcacatc cctggcccta atgcaccct	1034
gtcctggggt cgagcctgcg tccaggtcct ggaccgggaa gtccaagtgg cgaagcaaaa	1094
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taggtgggca ttgcggcctc cgcggtggac gtgttytttt ytaagccatg gagtgagtga	1454
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 <223> homology
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193


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194


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agggtaggga cttctccgc agcgacgcgg ctggcaagac tgtttgtgtt gcgggggccc      120
gaacttcaag gtgattttac aacgag atg ctg ctc tcc ata ggg atg ctc atg      173

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195

Met Leu Leu Ser Ile Gly Met Leu Met																
-30																
ctg	tca	gcc	aca	caa	gtc	tac	acc	atc	ttg	act	gtc	cag	ctc	ttt	gca	221
Leu	Ser	Ala	Thr	Gln	Val	Tyr	Thr	Ile	Leu	Thr	Val	Gln	Leu	Phe	Ala	
-25					-20					-15					-10	
ttc	tta	aac	cta	ctg	cct	gta	gaa	gca	gac	att	tta	gca	tat	aac	ttt	269
Phe	Leu	Asn	Leu	Leu	Pro	Val	Glu	Ala	Asp	Ile	Leu	Ala	Tyr	Asn	Phe	
				-5				1				5				
gaa	aat	gca	tct	cag	aca	ttt	gat	gac	ctc	ccc	gca	ara	ttt	ggg	tat	317
Glu	Asn	Ala	Ser	Gln	Thr	Phe	Asp	Asp	Leu	Pro	Ala	Xaa	Phe	Gly	Tyr	
	10						15				20					
aga	ctt	cca	gct	gaa	ggg	tta	aag	ggg	ttt	tta	att	aac	tca	aaa	cca	365
Arg	Leu	Pro	Ala	Glu	Gly	Leu	Lys	Gly	Phe	Leu	Ile	Asn	Ser	Lys	Pro	
	25					30					35					
gag	aat	gcc	tgt	gaa	ccc	ata	gtg	cct	cca	cca	gta	aaa	gac	aat	tca	413
Glu	Asn	Ala	Cys	Glu	Pro	Ile	Val	Pro	Pro	Pro	Val	Lys	Asp	Asn	Ser	
40					45					50					55	
tct	ggc	act	ttc	atc	gtg	tta	att	ara	ara	ctt	gat	tgt	aat	ttt	gat	461
Ser	Gly	Thr	Phe	Ile	Val	Leu	Ile	Xaa	Xaa	Leu	Asp	Cys	Asn	Phe	Asp	
				60					65					70		
ata	aag	gtt	tta	aat	gca	cag	aga	gca	gga	tac	aag	gca	gcc	ata	gtt	509
Ile	Lys	Val	Leu	Asn	Ala	Gln	Arg	Ala	Gly	Tyr	Lys	Ala	Ala	Ile	Val	
				75				80					85			
cac	aat	gtt	gat	tct	gat	gac	ctc	att	agc	atg	gga	tcc	aac	gac	att	557
His	Asn	Val	Asp	Ser	Asp	Asp	Leu	Ile	Ser	Met	Gly	Ser	Asn	Asp	Ile	
	90					95						100				
gag	gta	cta	aag	aaa	att	gac	att	cca	tct	gtc	ttt	att	ggg	gaa	tca	605
Glu	Val	Leu	Lys	Lys	Ile	Asp	Ile	Pro	Ser	Val	Phe	Ile	Gly	Glu	Ser	
	105					110					115					
tca	gct	agt	tct	ctg	aaa	gat	gaa	ttc	aca	tak	gaa	aaa	ggg	ggc	cac	653
Ser	Ala	Ser	Ser	Leu	Lys	Asp	Glu	Phe	Thr	Xaa	Glu	Lys	Gly	Gly	His	
120					125					130					135	
ctt	atc	tta	gtt	cca	gaa	ttt	agt	ctt	cct	ttg	gaa	tac	tac	cta	att	701
Leu	Ile	Leu	Val	Pro	Glu	Phe	Ser	Leu	Pro	Leu	Glu	Tyr	Tyr	Leu	Ile	
				140					145					150		
ccc	ttc	ctt	atc	atr	gtg	ggc	atc	tgt	ctc	atc	ttg	ata	gtc	att	ttc	749
Pro	Phe	Leu	Ile	Xaa	Val	Gly	Ile	Cys	Leu	Ile	Leu	Ile	Val	Ile	Phe	
				155				160					165			
atg	atc	aca	aaa	ttg	tcc	agg	gat	aga	cat	aga	gct	aga	aga	aac	aga	797
Met	Ile	Thr	Lys	Leu	Ser	Arg	Asp	Arg	His	Arg	Ala	Arg	Arg	Asn	Arg	
	170					175					180					
ctt	cgt	aaa	gat	caa	ctt	aag	aaa	ctt	cct	gta	cat	aaa	ttc	aag	aaa	845
Leu	Arg	Lys	Asp	Gln	Leu	Lys	Lys	Leu	Pro	Val	His	Lys	Phe	Lys	Lys	
	185					190					195					
gga	gat	gag	tat	gat	gta	tgt	gcc	att	tgt	ttg	gat	gag	tat	gaa	gat	893
Gly	Asp	Glu	Tyr	Asp	Val	Cys	Ala	Ile	Cys	Leu	Asp	Glu	Tyr	Glu	Asp	
200					205					210					215	
gga	gac	aaa	ctc	aga	atc	ctt	ccc	tgt	tcc	cat	gct	tat	cat	tgc	aag	941
Gly	Asp	Lys	Leu	Arg	Ile	Leu	Pro	Cys	Ser	His	Ala	Tyr	His	Cys	Lys	
				220					225					230		
tgt	gta	gac	cct	tgg	cta	act	aaa	acc	aaa	aaa	acc	tgt	cca	gtg	tgc	989
Cys	Val	Asp	Pro	Trp	Leu	Thr	Lys	Thr	Lys	Lys	Thr	Cys	Pro	Val	Cys	
			235					240					245			
agg	caa	aaa	gtt	gtt	cct	tct	caa	ggc	gat	tca	gac	tct	gac	aca	gac	1037
Arg	Gln	Lys	Val	Val	Pro	Ser	Gln	Gly	Asp	Ser	Asp	Ser	Asp	Thr	Asp	
	250						255				260					
agt	agt	caa	gaa	gaa	aat	gaa	gtg	aca	gaa	cat	acc	cct	tta	ctg	aga	1085
Ser	Ser	Gln	Glu	Glu	Asn	Glu	Val	Thr	Glu	His	Thr	Pro	Leu	Leu	Arg	

265	270	275	
cct tta gnc ttc tgt cag tgc cca rgt cam ttt ggg gct tta ntc gga			1133
Pro Leu Xaa Phe Cys Gln Cys Pro Xaa Xaa Phe Gly Ala Leu Xaa Gly			
280	285	290	295
ant ccc gct cac ant cag aak cat gac aga atc att cag act ast gag			1181
Xaa Pro Ala His Xaa Gln Xaa His Asp Arg Ile Ile Gln Thr Xaa Glu			
	300	305	310
gaa gac gac aat gaa gat act gac agt agt gat gca gaa gaa			1223
Glu Asp Asp Asn Glu Asp Thr Asp Ser Ser Asp Ala Glu Glu			
	315	320	325
tgaaattaat gaacatgatg tcgtgggtcca gttgcagcct aatgggtgaac gggattacaa			1283
catagcaaact actgtttgac tttcagaaga tgattggttt atttcccttt aaaatgatta			1343
ggatatatact gtaatttgat tttttgctcc cttaaaagat ttytgtagaa ataacttatt			1403
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tgccaagaat atacttcatt cactaataat agactggtgc tgtaactcaa gcatcaattc			1523
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agctccaaac ccatgaaaaa ttgccaagta taaaagcttc tcaagaatga g atg gat	117
	Met Asp
tct agg gtg tct tca cct gag aag caa gat aaa gag aat ttc gtg ggt	165
Ser Arg Val Ser Ser Pro Glu Lys Gln Asp Lys Glu Asn Phe Val Gly	
-40	-35
gtc aac aat aaa cgg ctt ggt gta tgt ggc tgg atc ctg ttt tcc ctc	213
Val Asn Asn Lys Arg Leu Gly Val Cys Gly Trp Ile Leu Phe Ser Leu	
	-20
tct ttc ctg ttg gtg atc att acc ttc ccc atc tcc ata tgg atg tgc	261
Ser Phe Leu Leu Val Ile Ile Thr Phe Pro Ile Ser Ile Trp Met Cys	
	-5
ttg aag atc att aag gag tat gaa cgt gct gtt gta ttc cgt ctg gga	309
Leu Lys Ile Ile Lys Glu Tyr Glu Arg Ala Val Val Phe Arg Leu Gly	
10	15
cgc atc caa gct gac aaa gcc aag ggg cca ggt ttg atc ctg gtc ctg	357
Arg Ile Gln Ala Asp Lys Ala Lys Gly Pro Gly Leu Ile Leu Val Leu	
25	30
cca tgc ata gat gtg ttt gtc aag gtt gac ctc cga aca gtt act tgc	405
Pro Cys Ile Asp Val Phe Val Lys Val Asp Leu Arg Thr Val Thr Cys	
	45
aac att cct cca caa gag atc ctc acc aga gac tcc gta act act cag	453
Asn Ile Pro Pro Gln Glu Ile Leu Thr Arg Asp Ser Val Thr Thr Gln	
	60
	65
	70

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1. The first part of the document is a list of names and addresses. The names are: John Doe, Jane Smith, and Bob Johnson. The addresses are: 123 Main St, 456 Elm St, and 789 Oak St.

2. The second part of the document is a list of names and addresses. The names are: Alice Brown, Charlie White, and David Green. The addresses are: 101 Main St, 202 Elm St, and 303 Oak St.

3. The third part of the document is a list of names and addresses. The names are: Eve Black, Frank Blue, and Grace Red. The addresses are: 404 Main St, 505 Elm St, and 606 Oak St.

4. The fourth part of the document is a list of names and addresses. The names are: Henry Yellow, Irene Purple, and Jack Orange. The addresses are: 707 Main St, 808 Elm St, and 909 Oak St.

5. The fifth part of the document is a list of names and addresses. The names are: Karen Pink, Larry Grey, and Mary Silver. The addresses are: 1010 Main St, 1111 Elm St, and 1212 Oak St.

gta gat gga gtt gtc tat tac aga atc tat agt gct gtc tca gca gtg	501
Val Asp Gly Val Val Tyr Tyr Arg Ile Tyr Ser Ala Val Ser Ala Val	
75 80 85	
gct aat gtc aac gat gtc cat caa gca aca ttt ctg ctg gct caa acc	549
Ala Asn Val Asn Asp Val His Gln Ala Thr Phe Leu Leu Ala Gln Thr	
90 95 100	
act ctg aga aat gtc tta ggg aca cag acc ttg tcc cag atc tta gct	597
Thr Leu Arg Asn Val Leu Gly Thr Gln Thr Leu Ser Gln Ile Leu Ala	
105 110 115 120	
gga cga gaa gag atc gcc cat agc atc cag act tta ctt gat gat gcc	645
Gly Arg Glu Glu Ile Ala His Ser Ile Gln Thr Leu Leu Asp Asp Ala	
125 130 135	
acc gaa ctg tgg ggg atc cgg gtg gcc cga gtg gaa atc aaa gat gtt	693
Thr Glu Leu Trp Gly Ile Arg Val Ala Arg Val Glu Ile Lys Asp Val	
140 145 150	
cgg att ccc gtg cag ttg cag aga tcc atg gca gcc gag gct gag gcc	741
Arg Ile Pro Val Gln Leu Gln Arg Ser Met Ala Ala Glu Ala Glu Ala	
155 160 165	
acc cgg gaa gcg aga gcc aag gtc ctt gca gct gaa gga gaa atg agt	789
Thr Arg Glu Ala Arg Ala Lys Val Leu Ala Ala Glu Gly Glu Met Ser	
170 175 180	
gct tcc aaa tcc ctg aag tca gcc tcc atg gtg ctg gct gag tct ccc	837
Ala Ser Lys Ser Leu Lys Ser Ala Ser Met Val Leu Ala Glu Ser Pro	
185 190 195 200	
ata gct ctc cag ctg cgc tac ctg cag acc ttg agc acg gta gcc acc	885
Ile Ala Leu Gln Leu Arg Tyr Leu Gln Thr Leu Ser Thr Val Ala Thr	
205 210 215	
gag aag aat tct acg att gtg ttt cct ctg ccc atg aat ata cta gag	933
Glu Lys Asn Ser Thr Ile Val Phe Pro Leu Pro Met Asn Ile Leu Glu	
220 225 230	
ggc att ggt ggc gtc agc tat gat aac cac aag aag ctt cca aat aaa	981
Gly Ile Gly Gly Val Ser Tyr Asp Asn His Lys Lys Leu Pro Asn Lys	
235 240 245	
gcc tgaggtcctc ttgcggtagt cagctaaaaa aaaaaaaaa	1022
Ala	

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199




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60

200

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ctggagttac	ttattaacat	caaggctgga	acctatttgc	ctcagtccta	tctgattc	238
atg agc aca	tgg tta tta	ctg atc gca	ttg aaa aca	ttg atc acc	tgg	286
Met Ser Thr	Trp Leu Leu	Leu Ile Ala	Leu Lys Thr	Leu Ile Thr	Trp	
-25		-20		-15		
gtt tct tta	ttt atc gac	tgt gtc atg	aca agg aaa	ctt aca aac	tgc	334
Val Ser Leu	Phe Ile Asp	Cys Val Met	Thr Arg Lys	Leu Thr Asn	Cys	
-10		-5	1	5		
aac gct aga	gaa act att	aaa ggt att	cag aaa cgt	gaa gcc agc	aat	382
Asn Ala Arg	Glu Thr Ile	Lys Gly Ile	Gln Lys Arg	Glu Ala Ser	Asn	
	10		15	20		
tgt ttc gca	att cgg cat	ttt gaa aac	aaa ttt gcc	gtg gaa act	tta	430
Cys Phe Ala	Ile Arg His	Phe Glu Asn	Lys Phe Ala	Val Glu Thr	Leu	
	25	30		35		
att tgt tct	tgaacagtca	agaaaaacat	tattgaggaa	aattaatc		479
Ile Cys Ser						
40						
acagcataac	cccacccttt	acattttgtg	cagtgattat	tttttaaagt	cttctttcat	539
gtaagtagca	aacagggtt	tactatcttt	tcatctcatt	aattcaatta	aaaccattac	599
ccccaaaaaa	aaaaaa					615

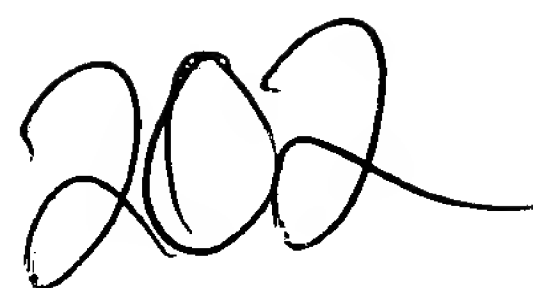
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201


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Ala	Gly	Leu	Ala	Asp	Met	Ala	Arg	Pro	Ala	Glu	Lys	Leu	Ser	Thr	Ala												
				-5					1			5															
caa	tct	gct	gtt	ttg	atg	gct	aca	ggg	ttt	att	tgg	tca	aga	tac	tca		414										
Gln	Ser	Ala	Val	Leu	Met	Ala	Thr	Gly	Phe	Ile	Trp	Ser	Arg	Tyr	Ser												
		10					15				20																
ctt	gta	att	att	ccg	aaa	aat	tgg	agt	ctg	ttt	gct	gtt	aat	ttc	ttt		462										
Leu	Val	Ile	Ile	Pro	Lys	Asn	Trp	Ser	Leu	Phe	Ala	Val	Asn	Phe	Phe												
		25				30				35																	
gtg	ggg	gca	gca	gga	gcc	tct	cag	ctt	ttt	cgt	att	tgg	aga	tat	aac		510										
Val	Gly	Ala	Ala	Gly	Ala	Ser	Gln	Leu	Phe	Arg	Ile	Trp	Arg	Tyr	Asn												
40					45				50					55													
caa	gaa	cta	aaa	gct	aaa	gca	cac	aaa	taaaagagtt	cctgatcacc							557										
Gln	Glu	Leu	Lys	Ala	Lys	Ala	His	Lys																			
				60																							
tga	aca	aat	ctt	agat	gtgg	ac	aaa	acc	attg	gg	ac	ct	tag	ttt	gg	tt	attg	ataa	617								
ag	caa	ag	cta	act	gtgt	gtt	tag	aagg	cac	tg	ta	act	ggt	ag	ct	agt	ttct	tg	attca	ata	677						
g	aaaa	at	gca	g	caa	act	ttt	a	ata	ac	ag	tc	tct	ct	ac	atg	act	ta	agg	aa	ctt	at	ct	atg	737		
g	at	att	ag	ta	g	a	c	att	ttt	gtc	c	g	t	a	a	t	a	a	a	a	a	a	a	a	a	a	797
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204


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205


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<222> 154..403
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cagccctgct ccctgcagcc aggtgtagtt tcgggagcca ctggggccaa agtgagagtc      120
cagcggtctt ccagcgcttg ggccacggcg gcggccctgg gagcagaggt ggagcgaccc      180
cattacgcta aag atg aaa ggc tgg ggt tgg ctg gcc ctg ctt ctg ggg      229
          Met Lys Gly Trp Gly Trp Leu Ala Leu Leu Leu Gly
          -20                      -15                      -10
gcc ctg ctg gga acc gcc tgg gct cgg agg agc cgg gat ctc cac tgt      277
Ala Leu Leu Gly Thr Ala Trp Ala Arg Arg Ser Arg Asp Leu His Cys
          -5                      1                      5
gga gca tgc agg gct ctg gtg gat gaa cta gaa tgg gaa att gcc cag      325
Gly Ala Cys Arg Ala Leu Val Asp Glu Leu Glu Trp Glu Ile Ala Gln
          10                      15                      20
gtg gac ccc aag aag acc att cag atg gga tcc ttc cgg atc aat cca      373
Val Asp Pro Lys Lys Thr Ile Gln Met Gly Ser Phe Arg Ile Asn Pro
          25                      30                      35                      40
gat ggc agc cag tca gtg gtg gag gta act gtt act gkt tcc ccc aaa      421
Asp Gly Ser Gln Ser Val Val Glu Val Thr Val Thr Xaa Ser Pro Lys

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206

	45	50	55	
aca aaa gta gct cac tct ggc ttt tgg atg aaa att cga ctg ctt aaa				469
Thr Lys Val Ala His Ser Gly Phe Trp Met Lys Ile Arg Leu Leu Lys				
	60	65	70	
aaa gga cct tgg tct taatagaaaa tgaagraaaa cagactcaga aaaaaagatt				524
Lys Gly Pro Trp Ser				
	75			
tbggctctgt ctcawtttgg aagaaggctg gcaggcttat tccccaatgc aactttgctt				584
cctggctgca aaccyttaat acytttgttt ctgctgtaga aatttggttag ccaaaacawg				644
ggagtcctga twcagcaacc ccttcttcca caatccacca tgactgggtt ttaatgtamc				704
acttggggta tacatgcaaa accatccggt cmaaaatctg aatycggagc ttaaaaattt				764
aaaaatgaaa aacchaaaaa aaaaaaaaa				792

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207


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208

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<222> 684..751

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<223> homology

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<220>

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<222> 2..172

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<220>

<221> misc_feature

<222> 743

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ccaaagtgcg agtccagcgg tcttccagcg cttgggccac ggcggcggcc ctgggagcag 120

aggtggagcg accccattac gctaaag atg aaa ggc tgg ggt tgg ctg gcc ctg 174

Met Lys Gly Trp Gly Trp Leu Ala Leu

-20

-15

ctt ctg ggg gcc ctg ctg gga acc gcc tgg gct cgg agg agc cag gat 222

Leu Leu Gly Ala Leu Leu Gly Thr Ala Trp Ala Arg Arg Ser Gln Asp

-10

-5

1

5

ctc cac tgt gga gca tgc agg gct ctg gtg gat gaa act aga atg gga 270

Leu His Cys Gly Ala Cys Arg Ala Leu Val Asp Glu Thr Arg Met Gly

10

15

20

aat tgc cca ggt gga ccc caa gaa gac cat tca gat ggg atc ttt ccg 318

Asn Cys Pro Gly Gly Pro Gln Glu Asp His Ser Asp Gly Ile Phe Pro

25

30

35

gat caa tcc aga tgg cag cca gtc agt ggt gga ggt gcc tta tgc ccg 366

Asp Gln Ser Arg Trp Gln Pro Val Ser Gly Gly Gly Ala Leu Cys Pro

40

45

50

ctc aga ggc cca cct cac aga gct gct gga gga gat atg tgaccggatg 415

Leu Arg Gly Pro Pro His Arg Ala Ala Gly Gly Asp Met

55

60

65

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ggccggaatg	gagaatccag	tgaactggac	ctacaaggca	tccgaatcga	ctcagatatt	535
agcggcaccc	tcaagbtttg	cgtgtgggaa	cattgtggag	gaatacgagg	atgaactcat	595
tgaattcttt	tcccgaagagg	ctgacaatgt	taaagacaaa	ctttgcagta	agcgaacaga	655
tctttgtgac	catgccctgc	acatatcggc	atgatgagct	atgaaccact	ggagcagccc	715
acactggcct	gatggatcac	ccccaggnaa	gggaaaatgg	tggcaatgcc	ttttatatat	775
tatgttttac	tgaaattaac	tgaaaaatat	gaaaccaaaa	gtscaaaaaa	aaaaaaa	832

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210


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ccctgcagtt cgcgwwacag tctctattag agcgcgtgta tagaggcaga kaggagtga      120
gtccacagtt cctctcctcc tagagcctgc cgacc atg ccc gcg ggc gtg ccc      173
                                Met Pro Ala Gly Val Pro
                                -25                                -20
atg tcc acc tac ctg aaa atg ttc gca gcc agt ctc ctg gcc atg tgc      221
Met Ser Thr Tyr Leu Lys Met Phe Ala Ala Ser Leu Leu Ala Met Cys
                                -15                                -10                                -5
gca ggg gca gaa gtg gtg cac agg tac tac cga ccg gac ctg aca ata      269
Ala Gly Ala Glu Val Val His Arg Tyr Tyr Arg Pro Asp Leu Thr Ile
                                1                                5                                10
cct gaa att cca cca aag cgt gga gaa ctc aaa acg gag ctt ttg gga      317
Pro Glu Ile Pro Pro Lys Arg Gly Glu Leu Lys Thr Glu Leu Leu Gly
                                15                                20                                25
ctg aaa gaa aga aaa cac aaa cct caa gtt tct caa cag gag gaa ctt      365
Leu Lys Glu Arg Lys His Lys Pro Gln Val Ser Gln Gln Glu Glu Leu
30                                35                                40                                45
aaa taactatgcc aagaattctg tgaataatat aagtcttaaa tatgtatttc      418
Lys
ttaatttatt gcatcaaact acttgtcctt aagcacttag tctaattgcta actgcaagag      478
gaggtgctca gtggatgttt agccgatacg ttgaaattta attacggttt gattgatatt      538
tcttgaaaac tgccaaagca catatcatca aaccatttca tgaatatggt ttggaagatg      598
tttagtcttg aatataacgc gaaatagaat atttgtaagt ctactatatg gggtgtcttt      658
atttcatata aattaagaaa ttatttaaaa actatgaact aggttttcatt aaaaaaaaaa      718
gaa                                                                    721

<210> 66
<211> 531
<212> DNA

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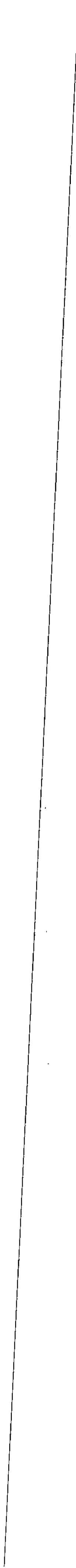


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<213> Homo sapiens
<220>
<221> sig_peptide
<222> 272..397
<223> Von Heijne matrix
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      seq RIPS L P G S P V C W A / W P
<220>
<221> polyA_signal
<222> 503..508
<220>
<221> polyA_site
<222> 518..531
<220>
<221> misc_feature
<222> 235..517
<223> homology
      id :AA524403
      est
<220>
<221> misc_feature
<222> 52..208
<223> homology
      id :AA524403
      est
<220>
<221> misc_feature
<222> 259..517
<223> homology
      id :N93600
      est
<220>
<221> misc_feature
<222> 85..207
<223> homology
      id :N93600
      est
<220>
<221> misc_feature
<222> 353..517
<223> homology
      id :AA594610
      est
<220>
<221> misc_feature
<222> 258..363
<223> homology
      id :AA594610
      est
<220>
<221> misc_feature
<222> 105..207
<223> homology
      id :AA594610
      est
<220>
<221> misc_feature
<222> 202..517

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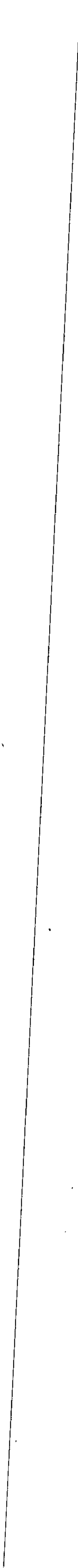
213



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<223> homology
      id :AA074748
      est
<220>
<221> misc_feature
<222> 116..153
<223> homology
      id :AA074748
      est
<220>
<221> misc_feature
<222> 167..202
<223> homology
      id :AA074748
      est
<220>
<221> misc_feature
<222> 258..517
<223> homology
      id :N93603
      est
<220>
<221> misc_feature
<222> 208..251
<223> homology
      id :N93603
      est
<220>
<221> misc_feature
<222> 163..202
<223> homology
      id :N93603
      est
<220>
<221> misc_feature
<222> 90..125
<223> homology
      id :N93603
      est
<220>
<221> misc_feature
<222> 125..363
<223> homology
      id :HSPD04938
      est
<220>
<221> misc_feature
<222> 353..517
<223> homology
      id :HSPD04938
      est
<220>
<221> misc_feature
<222> 28..227
<223> homology
      id :AA074804
      est
<220>

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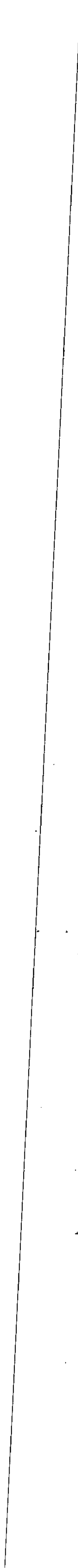
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<221> misc_feature
<222> 265..310
<223> homology
      id :AA074804
      est
<220>
<221> misc_feature
<222> 227..263
<223> homology
      id :AA074804
      est
<220>
<221> misc_feature
<222> 352..385
<223> homology
      id :AA074804
      est
<400> 66
aaaaggaaag aggtysggag cgctcgcgag atctcggacc acccaacctg aaaggtgctt      60
aggaagttga aaggcccaga ggaggcctcc gggcaaattg ccggagctgg accgaccatg      120
ctgctacgag aagagaatgg ctgttgcagt cggcgtcaga gcagctccag tgccggggat      180
tcggacggag agcgcgagga ctcggcggct gagcgcgccc gacagcagct agaggcgctg      240
ctcaacaaga ctatgcgcat tcgcatgaca g atg gac gga cac tgg tcg gct      292
                               Met Asp Gly His Trp Ser Ala
                               -40
gct ttc tct gca ctg acc gtg act gca atg tca tcc tgg gct cgg cgc      340
Ala Phe Ser Ala Leu Thr Val Thr Ala Met Ser Ser Trp Ala Arg Arg
-35                               -30                               -25                               -20
agg agt tcc tca agc cgt cgg att cct tct ctg ccg ggg agc ccc gtg      388
Arg Ser Ser Ser Ser Arg Arg Ile Pro Ser Leu Pro Gly Ser Pro Val
                               -15                               -10                               -5
tgc tgg gcc tgg cca tgg tac ccg gac acc aca tcg ttt cca ttg agg      436
Cys Trp Ala Trp Pro Trp Tyr Pro Asp Thr Thr Ser Phe Pro Leu Arg
                               1                               5                               10
tgc aga ggg aga gtc tgaccgggcc tccgtatctc tgaccacgat ggcgcttacc      491
Cys Arg Gly Arg Val
15
tttcagactt cattaaactt atgaccaaaa aaaaaaaaaa      531

<210> 67
<211> 783
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 381..629
<223> Von Heijne matrix
      score 8.60000038146973
      seq LELLTSCSPASA/SQ
<220>
<221> polyA_signal
<222> 736..741
<220>
<221> polyA_site
<222> 770..783
<220>
<221> misc_feature
<222> 207..263

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215



<223> homology

id :AA357230

est

<400> 67

agggacttcc	ggcctcgctg	gcgtggacgt	ttgtggtggg	gcgtggttgg	ccgcgctctc	60
agaactgtgc	tgggaaggat	ggtagggcga	ctggggctca	cctccgcacc	gttgtaggac	120
ccggggtagg	gttttgagcc	cgtgggagct	gccccacgcg	gcctcgctct	gccaacggtc	180
ggatggcgga	gacgaaggac	gcagcgcaga	tggttggtgac	cttcaaggat	gtggctgtga	240
cctttacccg	ggaggagtgg	agacagctgg	acctggccca	gaggaccctg	taccgagagg	300
tgatcggggt	cccaaaccag	agttggtcca	cctgctagag	catgggcagg	agctgtggat	360
agtgaagaga	ggcctctcac	atg cta cct	gtg cag agt	ttc act ctt	gtt gcc	413

Met Leu Pro Val Gln Ser Phe Thr Leu Val Ala

-80

-75

cag gct gga	gtg cag tgg	cgc cat ctc	agc tca ctg	caa ctt ctg	cct	461
Gln Ala Gly	Val Gln Trp	Arg His Leu	Ser Ser Leu	Gln Leu Leu	Pro	

-70

-65

-60

ccc gag ttc	aag gga ttc	tcc tgc ctc	agc ctc ccg	agt agc tgg	gat	509
Pro Glu Phe	Lys Gly Phe	Ser Cys Leu	Ser Leu Pro	Ser Ser Trp	Asp	

-55

-50

-45

tac agg cgc	cca cca cca	tgc ccg gct	ggt ttt ttt	gta ttt tta	gta	557
Tyr Arg Arg	Pro Pro Pro	Cys Pro Ala	Gly Phe Phe	Val Phe Leu	Val	

-40

-35

-30

-25

gag acg ggg	ctt cac cat	gtt ggc cag	gct ggt ctt	gaa ctc ttg	acc	605
Glu Thr Gly	Leu His His	Val Gly Gln	Ala Gly Leu	Glu Leu Leu	Thr	

-20

-15

-10

tca tgt agt	cca ccc gcc	tct gcc tcc	caa agt gct	gcg att aca	ggc	653
Ser Cys Ser	Pro Pro Ala	Ser Ala Ser	Gln Ser Ala	Ala Ala Ile	Thr Gly	

-5

1

5

gtg agc cac	gtg ccc ggc	aaa aaa aaa	ctg ctt aag	ggt gaa aag	aaa	701
Val Ser His	Val Pro Gly	Lys Lys Lys	Leu Leu Lys	Val Glu Lys	Lys	

10

15

20

aat tta aga	aaw ttg ctg	acg gra ata	aaa acy taataaaaact	accacccgaa	754
Asn Leu Arg	Xaa Leu Leu	Thr Xaa Ile	Lys Thr		

25

30

35

ggaatgaaaa	aaccaaaaaa	aaaaaaaaaa	783
------------	------------	------------	-----

<210> 68

<211> 996

<212> DNA

<213> Homo sapiens

<220>

<221> sig_peptide

<222> 140..205

<223> Von Heijne matrix

score 5.90000009536743

seq IILGCLALFLLQ/RK

<220>

<221> polyA_signal

<222> 965..970

<220>

<221> polyA_site

<222> 984..996

<220>

<221> misc_feature

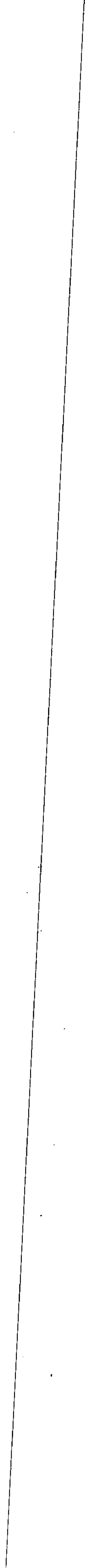
<222> 676..959

<223> homology

id :AA399103

est

216



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<220>
<221> misc_feature
<222> 609..679
<223> homology
      id :AA399103
      est

<220>
<221> misc_feature
<222> 225..433
<223> homology
      id :AA398040
      est

<220>
<221> misc_feature
<222> 433..563
<223> homology
      id :AA398040
      est

<400> 68
aacagttacg aaggagagct gcaaaagttg cagcagaaag gttgggagtc cgcacaggtt      60
ccgtagccca cagaaaagaa gcaagggacg gcaggactgt ttcacacttt tctgcttctg      120
gaaggtgctg gacaaaaac atg gaa cta att tcc cca aca gtg att ata atc      172
                Met Glu Leu Ile Ser Pro Thr Val Ile Ile Ile
                        -20                                -15

ctg ggt tgc ctt gct ctg ttc tta ctc ctt cag cgg aag aat ttg cgc      220
Leu Gly Cys Leu Ala Leu Phe Leu Leu Leu Gln Arg Lys Asn Leu Arg
      -10                                -5                                1                                5
aga ccc ccg tgc atc aag ggc tgg att cct tgg att gga gtt gga ttt      268
Arg Pro Pro Cys Ile Lys Gly Trp Ile Pro Trp Ile Gly Val Gly Phe
                        10                                15                                20
gak ttt ggg aaa gcc cct cta gaa ttt ata gag aaa gca aga atc aag      316
Xaa Phe Gly Lys Ala Pro Leu Glu Phe Ile Glu Lys Ala Arg Ile Lys
                        25                                30                                35
gtā tgt ggt cgt ggc ava cgg ggt ctc cag agg aga caa tgc ttt ctt      364
Val Cys Gly Arg Gly Xaa Arg Gly Leu Gln Arg Arg Gln Cys Phe Leu
      40                                45                                50
ttt taaactttct ttcattgact cttaagtgcg gggctagaac acggggaaca      417
Phe

tacctgcttg cctcaaacta aaggatctag tcmtytctga akteectctac tsacrtrtra      477
caacaatatc ctgtgcaaaa ttttgcgaaa gaaatgaaat acaattgcmg cgtgcatcga      537
cattttttgga agtagagatt aacyyttcgt attttttactt cmtcgaagtt aagttccaaa      597
tgtgtatgtg ttaagtaaat gtttttcagta aytgggaaag ataaagtgtg atccaattta      657
agttttgtgaa aatgagtaat tccgtatcca aaytggagtt aacaccaaag tattgtacaa      717
attgcttgca cagttgggcc gtacacaata gacaggctyt gtatttttag ctgacgttgt      777
tatttgatga tgatgtactc cattttcamt acggcccgaa gagamtagta atcctccttg      837
tagtagatgt ttttgtcttg aaagtatctt ttaaagttyt gagcacttta aggaacagac      897
ccttattaat gtyttttaag ttttattcaa tttccagtca caaatatttt atggtatttg      957
attgtytaat aaatttgtat gatattaaaa aaaaaaaaaa      996


<210> 69
<211> 657
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 183..338
<223> Von Heijne matrix
      score 3.79999995231628

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seq VMLETCGLLVSLG/QS
<220>
<221> polyA_signal
<222> 620..625
<220>
<221> polyA_site
<222> 644..657
<220>
<221> misc_feature
<222> 207..263
<223> homology
      id :AA357230
      est
<400> 69
agggaacttcc ggccctcgctg gcgtggacgt ttgtggtggg gcgtggtggt ccgcgctctc      60
agaactgtgc tgggaaggat ggtagggcga ctggggctca cctccgcacc gttgtaggac      120
ccggggtagg gttttgagcc cgtgggagct gccccacgcg gcctcgctct gccaacggtc      180
gg atg gcg gag acg aag gac gca gcg cag atg ttg gtg acc ttc aag      227
  Met Ala Glu Thr Lys Asp Ala Ala Gln Met Leu Val Thr Phe Lys
      -50              -45              -40
gat gtg gct gtg acc ttt acc cgg gag gag tgg aga cag ctg gac ctg      275
Asp Val Ala Val Thr Phe Thr Arg Glu Glu Trp Arg Gln Leu Asp Leu
      -35              -30              -25
gcc cag agg acc ctg tac cga gag gtg atg ctg gag acc tgt ggg ctt      323
Ala Gln Arg Thr Leu Tyr Arg Glu Val Met Leu Glu Thr Cys Gly Leu
      -20              -15              -10
ctg gtt tca cta ggg caa agc att tgg ctg cat ata aca gaa aac cag      371
Leu Val Ser Leu Gly Gln Ser Ile Trp Leu His Ile Thr Glu Asn Gln
      -5              1              5              10
atc aaa ctg gct tca cct gga agg aaa ttc act aac tcg cct gat gag      419
Ile Lys Leu Ala Ser Pro Gly Arg Lys Phe Thr Asn Ser Pro Asp Glu
      15              20              25
aag cct gag gtg tgg ttg gct cca ggc ctg ttc ggt gcc gca gcc cag      467
Lys Pro Glu Val Trp Leu Ala Pro Gly Leu Phe Gly Ala Ala Ala Gln
      30              35              40
tgacgccatc aaggatgtct tggttctctg ttccttcttc ttggttcagg cttctggatt      527
gtcctcaggc tggctcctca tagggatgct ggggtgctgca gccttgactg gggcagcagg      587
cccccatggt tcaatccatc ctcccacctt ggaataaatg ctttcttttc acaatgagaa      647
aaaaaaaaaa      657

<210> 70
<211> 416
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 140..205
<223> Von Heijne matrix
      score 5.90000009536743
      seq IILGCLALFLLQ/RK
<220>
<221> polyA_signal
<222> 383..388
<220>
<221> polyA_site
<222> 405..416
<220>
<221> misc_feature

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218


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<222> 225..316
<223> homology
      id :AA398040
      est
<400> 70
aacagttacg aaggagagct gcaaaagttg cagcagaaag gttgggagtc cgcacaggtt      60
ccgtagccca cagaaaagaa gcaagggacg gcaggactgt ttcacacttt tctgcttctg      120
gaaggtgctg gacaaaaac atg gaa cta att tcc cca aca gtg att ata atc      172
              Met Glu Leu Ile Ser Pro Thr Val Ile Ile Ile
              -20                               -15
ctg ggt tgc ctt gct ctg ttc tta ctc ctt cag cgg aag aat ttg cgc      220
Leu Gly Cys Leu Ala Leu Phe Leu Leu Leu Gln Arg Lys Asn Leu Arg
      -10                               -5                               1                               5
aga ccc ccg tgc atc aag ggc tgg att cct tgg att gga gtt gga ttt      268
Arg Pro Pro Cys Ile Lys Gly Trp Ile Pro Trp Ile Gly Val Gly Phe
              10                               15                               20
gag ttt ggg aaa gcc cct cta gaa ttt ata gag aaa gca aga atc aag      316
Glu Phe Gly Lys Ala Pro Leu Glu Phe Ile Glu Lys Ala Arg Ile Lys
              25                               30                               35
tat gga cca ata ttt aca gtc ttt gct atg gga aac cga atg acc ttt      364
Tyr Gly Pro Ile Phe Thr Val Phe Ala Met Gly Asn Arg Met Thr Phe
              40                               45                               50
gtt act gaa gaa gga agg aat taatgtgttt ctaaaatcca aaaaaaaaaa a      416
Val Thr Glu Glu Gly Arg Asn
              55                               60

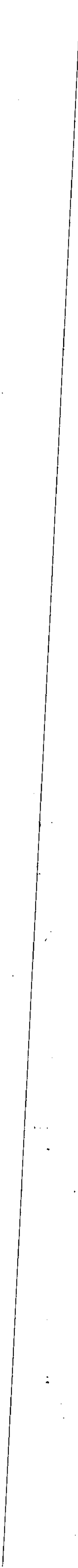
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<210> 71
<211> 543
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 129..176
<223> Von Heijne matrix
      score 4.80000019073486
      seq SLFIYIFLTCSNT/SP
<220>
<221> polyA_signal
<222> 513..518
<220>
<221> polyA_site
<222> 530..543
<220>
<221> misc_feature
<222> 264..500
<223> homology
      id :AA534039
      est
<220>
<221> misc_feature
<222> 205..315
<223> homology
      id :T82645
      est
<220>
<221> misc_feature
<222> 295..382
<223> homology

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219

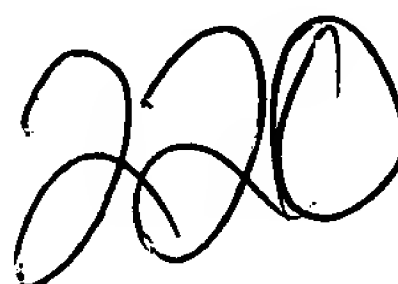


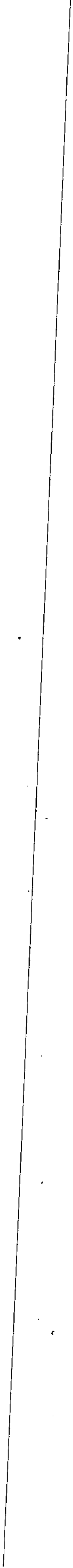

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id :T82645
est
<220>
<221> misc_feature
<222> 375..405
<223> homology
      id :T82645
      est
<220>
<221> misc_feature
<222> 50
<223> n=a, g, c or t
<400> 71
actgtcccat tcctccccct acaacacaca cacctttcag gcagggasgn gatgagcttc      60
cagccccaag agtggaggct gccacatcct aacatasgta tctattgaaa aggaagcagt      120
gtgtatct atg att ata tct ctg ttc atc tat ata ttt ttg aca tgt agc      170
      Met Ile Ile Ser Leu Phe Ile Tyr Ile Phe Leu Thr Cys Ser
            -15                -10                -5
aac acc tct cca tct tat caa gga act caa ctc ggt ctg ggt ctc ccc      218
Asn Thr Ser Pro Ser Tyr Gln Gly Thr Gln Leu Gly Leu Gly Leu Pro
            1                5                10
agt gcc cag tgg tgg cct ttg aca ggt agg agg atg cag tgc tgc agg      266
Ser Ala Gln Trp Trp Pro Leu Thr Gly Arg Arg Met Gln Cys Cys Arg
            15                20                25                30
cta ttt tgt ttt ttg tta caa aac tgt ctt ttc cct ttt ccc ctc cac      314
Leu Phe Cys Phe Leu Leu Gln Asn Cys Leu Phe Pro Phe Pro Leu His
            35                40                45
ctg att cag cat gat ccc tgt gag ctg gtt ctc aca atc tcc tgg gac      362
Leu Ile Gln His Asp Pro Cys Glu Leu Val Leu Thr Ile Ser Trp Asp
            50                55                60
tgg gct gag gca ggg gct tcg ctc tat tct ccc taaccatact gtcttccttt      415
Trp Ala Glu Ala Gly Ala Ser Leu Tyr Ser Pro
            65                70
cccccttgcc acttagcagt tatcccccca gctatgcctt ctccctccct cccttgccct      475
ggcatatatatt gtgccttatt tatgctgcaa atataacatt aaactatcaa gtgaaaaaaaa      535
aaaaaaaaa                                     .. 543

<210> 72
<211> 605
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 285..341
<223> Von Heijne matrix
      score 5.59999990463257
      seq PTLCVSSSPALWA/AS
<220>
<221> polyA_signal
<222> 575..580
<220>
<221> polyA_site
<222> 592..605
<220>
<221> misc_feature
<222> 53..296
<223> homology
      id :W07033

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```

      est
<220>
<221> misc_feature
<222> 348..432
<223> homology
      id :W07033
      est
<220>
<221> misc_feature
<222> 435..497
<223> homology
      id :W07033
      est
<220>
<221> misc_feature
<222> 293..337
<223> homology
      id :W07033
      est
<220>
<221> misc_feature
<222> 521..560
<223> homology
      id :W07033
      est
<220>
<221> misc_feature
<222> 489..520
<223> homology
      id :W07033
      est
<220>
<221> misc_feature
<222> 15..337
<223> homology
      id :AA151004
      est
<220>
<221> misc_feature
<222> 348..412
<223> homology
      id :AA151004
      est
<220>
<221> misc_feature
<222> 434..485
<223> homology
      id :AA151004
      est
<220>
<221> misc_feature
<222> 83..324
<223> homology
      id :AA476506
      est
<220>
<221> misc_feature
<222> 347..560

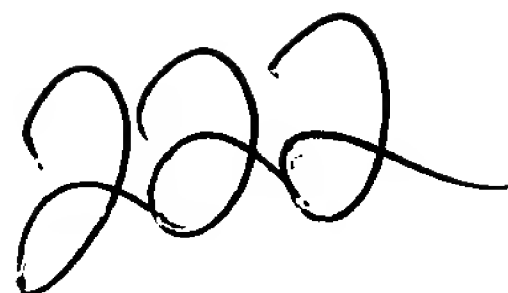
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221


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<223> homology
      id :AA476506
      est
<220>
<221> misc_feature
<222> 16..347
<223> homology
      id :W56567
      est
<220>
<221> misc_feature
<222> 350..405
<223> homology
      id :W56567
      est
<220>
<221> misc_feature
<222> 433..470
<223> homology
      id :W56567
      est
<220>
<221> misc_feature
<222> 15..296
<223> homology
      id :AA147584
      est
<220>
<221> misc_feature
<222> 348..421
<223> homology
      id :AA147584
      est
<220>
<221> misc_feature
<222> 293..337
<223> homology
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      est
<220>
<221> misc_feature
<222> 419..453
<223> homology
      id :AA147584
      est
<220>
<221> misc_feature
<222> 2..338
<223> homology
      id :AA281959
      est
<220>
<221> misc_feature
<222> 350..432
<223> homology
      id :AA281959
      est
<400> 72

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aacgcctwta agacagcgga actaagaaaa gaagaggcct gtggacagaa caatcatgtc      60
tgactccctg gtggtgtgcg aggtagaccc agagctaaca gaaaagctga kgaaattccg      120
cttccgaaaa gagacagaca atgcagccat cataatgaag gtggacaaag accggcagat      180
ggtggtgctg gaggaagaat ttcagaacat ttccccagag gagctcaaaa tggagttgcc      240
ggagagacag cccagggttcg tggtttacag ctacaagtac gtgc atg acg atg gcc      296
                                     Met Thr Met Ala
gag tgt cct acc ctt tgt gtt tca tct tct cca gcc ctg tgg gct gca      344
Glu Cys Pro Thr Leu Cys Val Ser Ser Ser Pro Ala Leu Trp Ala Ala
-15                               -10                               -5                               1
agc gaa aca aca gat gat gta tgc agg gag taaaaacagg ctggtgcaga      394
Ser Glu Thr Thr Asp Asp Val Cys Arg Glu
                    5                               10
cagcagagct cacaaagggtg ttcgaaatcc gcaccactga tgacctcact gaggcctggc      454
tccaagaaaa gttgtctttc tttcgttgat ctctgggctg gggactgaat tcctgatgtc      514
tgagtcctca aggtgactgg ggacttggaa cccctaggac ctgaacaacc aaggacttta      574
aataaatttt aaaatgcaaa aaaaaaaaaa a      605

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<210> 73
<211> 864
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 136..444
<223> Von Heijne matrix
      score 4.90000009536743
      seq VYAFLGLTAPSGS/KE
<220>
<221> polyA_signal
<222> 835..840
<220>
<221> polyA_site
<222> 851..864
<220>
<221> misc_feature
<222> 222..456
<223> homology
      id :AA136758
      est
<220>
<221> misc_feature
<222> 557..648
<223> homology
      id :AA136758
      est
<220>
<221> misc_feature
<222> 501..571
<223> homology
      id :AA136758
      est
<220>
<221> misc_feature
<222> 130..456
<223> homology
      id :AA393612
      est
<220>

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<221> misc_feature
<222> 88..130
<223> homology
      id :AA393612
      est
<220>
<221> misc_feature
<222> 501..538
<223> homology
      id :AA393612
      est
<220>
<221> misc_feature
<222> 130..458
<223> homology
      id :R59039
      est
<220>
<221> misc_feature
<222> 71..130
<223> homology
      id :R59039
      est
<220>
<221> misc_feature
<222> 557..716
<223> homology
      id :W48624
      est
<220>
<221> misc_feature
<222> 365..456
<223> homology
      id :W48624
      est
<220>
<221> misc_feature
<222> 501..571
<223> homology
      id :W48624
      est
<220>
<221> misc_feature
<222> 716..751
<223> homology
      id :W48624
      est
<220>
<221> misc_feature
<222> 222..458
<223> homology
      id :AA136810
      est
<220>
<221> misc_feature
<222> 501..581
<223> homology
      id :AA136810

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224


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      est
<220>
<221> misc_feature
<222> 587..668
<223> homology
      id :AA136810
      est
<220>
<221> misc_feature
<222> 130..419
<223> homology
      id :T35647
      est
<220>
<221> misc_feature
<222> 59..130
<223> homology
      id :T35647
      est
<220>
<221> misc_feature
<222> 557..852
<223> homology
      id :HUM093F06A
      est
<220>
<221> misc_feature
<222> 501..571
<223> homology
      id :HUM093F06A
      est
<220>
<221> misc_feature
<222> 130..384
<223> homology
      id :T35666
      est

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<400> 73
aaagttctcc ttccaccttc ccccaccctt ctctgccaac cgctgtttca gcccctagct      60
ggattccagc cattgctgca gctgctccac agcccttttc aggacccaaa caaccgcagc      120
cgctgttccc caggr atg gtg atc cgt gta tat att gca tct tcc tct ggc      171
          Met Val Ile Arg Val Tyr Ile Ala Ser Ser Ser Gly
                    -100                                -95

tct aca gcg att aag aag aaa caa caa gat gtg ctt ggt ttc cta gaa      219
Ser Thr Ala Ile Lys Lys Lys Gln Gln Asp Val Leu Gly Phe Leu Glu
      -90                                -85                                -80

gcc aac aaa ata gga ttt gaa gaa aaa gat att gca gcc aat gaa gag      267
Ala Asn Lys Ile Gly Phe Glu Glu Lys Asp Ile Ala Ala Asn Glu Glu
      -75                                -70                                -65                                -60

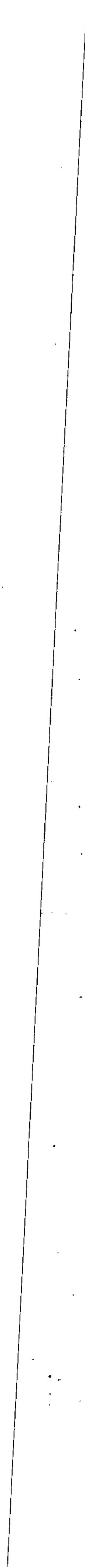
aat cgg aag tgg atg aga gaa aat gta cct gaa aat agt cga cca gcc      315
Asn Arg Lys Trp Met Arg Glu Asn Val Pro Glu Asn Ser Arg Pro Ala
                    -55                                -50                                -45

aca ggt aac ccc ctg cca cct cag att ttc aat gaa agc cag tat cgc      363
Thr Gly Asn Pro Leu Pro Pro Gln Ile Phe Asn Glu Ser Gln Tyr Arg
                    -40                                -35                                -30

ggg gac tat gat gcc ttc ttt gaa gcc aga gaa aat aat gca gtg tat      411
Gly Asp Tyr Asp Ala Phe Phe Glu Ala Arg Glu Asn Asn Ala Val Tyr
      -25                                -20                                -15

```





gcc ttc tta ggc ttg aca gcc cca tct ggt tca aag gaa gca gga agg	459
Ala Phe Leu Gly Leu Thr Ala Pro Ser Gly Ser Lys Glu Ala Gly Arg	
-10 -5 1 5	
tgc aag caa agc agc aag cca tgaaccttga gcactgtgct ttttaagcatc	510
Cys Lys Gln Ser Ser Lys Pro	
10	
ctgaaaaatg agtctccatt gctttttataa aatagcagaa ttagctttgc sttcaaaaga	570
aataggstta atgttgaaat aatagattag ttgggttttc acatgcaaac amtcaaaatg	630
aatacaaaat taaaattttga acattatggg gattatgggt aggagaatgg gatattaaca	690
taaaattata ttaataagta gatatygtag aaatagtgtt gttacctgcc aagccatcct	750
gtatacacca atgattttac aaagaaaaca cccttccttc cttytgccat tamtatggca	810
acctaagtgt atytgcagct ttacattaaa aaggagaaag agaaaaaaaaaaaa	864

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<210> 74
<211> 1033
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 200..427
<223> Von Heijne matrix
      score 4.69999980926514
      seq LIVYLVVVSFIAS/SS
<220>
<221> polyA_signal
<222> 1001..1006
<220>
<221> polyA_site
<222> 1022..1033
<220>
<221> misc_feature
<222> 55..406
<223> homology
      id :AA056667
      est
<220>
<221> misc_feature
<222> 397..487
<223> homology
      id :AA056667
      est
<220>
<221> misc_feature
<222> 527..584
<223> homology
      id :AA056667
      est
<220>
<221> misc_feature
<222> 482..531
<223> homology
      id :AA056667
      est
<220>
<221> misc_feature
<222> 581..634
<223> homology
      id :AA056667

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226


```

      est
<220>
<221> misc_feature
<222> 397..700
<223> homology
      id :AA044187
      est
<220>
<221> misc_feature
<222> 222..406
<223> homology
      id :AA044187
      est
<220>
<221> misc_feature
<222> 693..748
<223> homology
      id :AA044187
      est
<220>
<221> misc_feature
<222> 68..406
<223> homology
      id :AA131958
      est
<220>
<221> misc_feature
<222> 397..517
<223> homology
      id :AA131958
      est
<220>
<221> misc_feature
<222> 510..558
<223> homology
      id :AA131958
      est
<220>
<221> misc_feature
<222> 77..531
<223> homology
      id :W95957
      est
<220>
<221> misc_feature
<222> 527..558
<223> homology
      id :W95957
      est
<220>
<221> misc_feature
<222> 397..586
<223> homology
      id :AA041216
      est
<220>
<221> misc_feature
<222> 286..406

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227

<223> homology
id :AA041216
est

<220>

<221> misc_feature

<222> 582..700

<223> homology
id :AA041216
est

<220>

<221> misc_feature

<222> 77..406

<223> homology
id :W95790
est

<220>

<221> misc_feature

<222> 397..539

<223> homology
id :W95790
est

<220>

<221> misc_feature

<222> 474..760

<223> homology
id :AA461134
est

<220>

<221> misc_feature

<222> 788..940

<223> homology
id :AA461134
est

<400> 74

aagacgaggt	catgaatcat	gtgacggtgg	cttgaggagg	aacctgtctt	taaagctgtc	60
cctgaagtga	cagcggagag	aaccaggcag	cccagaaacc	ccaggcgtgg	agattgatcc	120
tgcgagagaa	gggggttcat	catggcggat	gacctaaagc	gattcttgta	taaaaagtta	180
ccaagtgttg	aagggtctcc	atg cca ttg	ttg tgt cag	ata gag atg	gag tac	232
		Met Pro Leu	Leu Cys Gln	Ile Glu Met	Glu Tyr	
		-75		-70		

ctg tta tta	aag tgg	caa atg	aca atg	ctc cag	agc atg	ctt tgc	gac	280
Leu Leu Leu	Lys Trp	Gln Met	Thr Met	Leu Gln	Ser Met	Leu Cys	Asp	
-65		-60		-55		-50		

ctg gtt tct	tat cca	ctt ttg	ccc ttg	caa cag	acc aag	gaa gca	aac	328
Leu Val Ser	Tyr Pro	Leu Leu	Pro Leu	Gln Gln	Thr Lys	Glu Ala	Asn	
	-45		-40		-35			

ttg gac ttt	cca aaa	ata aaa	gta tca	tct gtt	act ata	aca cct	acc	376
Leu Asp Phe	Pro Lys	Ile Lys	Val Ser	Ser Val	Thr Ile	Thr Pro	Thr	
	-30		-25		-20			

agg tgg ttc	aat tta	atc gtt	tac ctt	tgg gtg	gtg agt	ttc ata	gcc	424
Arg Trp Phe	Asn Leu	Ile Val	Tyr Leu	Trp Val	Val Ser	Phe Ile	Ala	
	-15		-10		-5			

agc agc agt	gcc aat	aca gga	cta att	gtc agc	cta gaa	aag gaa	ctt	472
Ser Ser Ser	Ala Asn	Thr Gly	Leu Ile	Val Ser	Leu Glu	Lys Glu	Leu	
1	5		10		15			


gct cca ttg	ttt gaa	gaa ctg	aga caa	ggt gtg	gaa gtt	tct	514
Ala Pro Leu	Phe Glu	Glu Leu	Arg Gln	Val Val	Glu Val	Ser	
	20		25				

taatctgaca	gtggtttcag	tgtgtacctt	atcttcatta	taacaacaca	atatcaatcc	574
agcaatcttt	agactacaat	aatactttta	tccatgtgct	caagaaaggg	cccctttttc	634
caacttatac	taaagagcta	gcatatagat	gtaatttata	gatagatcag	ttgctatatt	694
ttctgggtgta	gggtctttct	tatttagtga	gatctaggga	taccacagaa	atggttcagt	754
ctatcaacag	ctcccatgga	gttagtctgg	tcacagatat	ggatgagaga	ttytattcag	814
tggatcagaa	tcaaactggg	acattgatcc	acttgagccg	ttaagtgctg	ccaattgtac	874
aatatgccca	ggcttgcaga	ataaagccaa	ctttttattg	tgaataataa	taaggacata	934
tttttyttca	gattatgttt	tatttytttg	cattgagtga	ggaacataaa	atggcttggt	994
aaaagtaata	aatcagttac	aatcactaaa	aaaaaaaaa			1033

<210> 75
 <211> 499
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> sig_peptide
 <222> 68..133
 <223> Von Heijne matrix
 score 9.80000019073486
 seq LVVFCLALQLVPG/SP
 <220>
 <221> polyA_signal
 <222> 472..477
 <220>
 <221> polyA_site
 <222> 490..499
 <400> 75

aaacagcagt	gcctgggtcaa	acccagcaac	ccttggccag	aacttactca	cccatcccac	60
tgacacc	atg aag cct	gtg ctg cct	ctc cag ttc	ctg gtg gtg	ttc tgc	109
	Met Lys Pro	Val Leu Pro	Leu Gln Phe	Leu Val Val	Phe Cys	
	-20		-15		-10	
cta gca	ctg cag	ctg gtg	cct ggg	agt ccc	aag cag	157
Leu Ala	Leu Gln	Leu Val	Pro Gly	Ser Pro	Lys Gln	
	-5		1		5	
tat atc	ttg gaa	cct cca	ccc tgc	ata tca	gca cct	205
Tyr Ile	Leu Glu	Pro Pro	Pro Cys	Ile Ser	Ala Pro	
10		15		20		
cac ctg	tgt aca	atg cag	gaa gat	tgc gag	aaa gga	253
His Leu	Cys Thr	Met Gln	Glu Asp	Cys Glu	Lys Gly	
25		30		35		
tcc tcc	ttc tgt	ggg ata	gtc tgt	tca tca	gaa aca	301
Ser Ser	Phe Cys	Gly Ile	Val Cys	Ser Ser	Glu Thr	
	45		50		55	
aac aga	atc aaa	cac aag	ggc tca	gaa gtc	atc atg	346
Asn Arg	Ile Lys	His Lys	Gly Ser	Glu Val	Ile Met	
	60		65		70	
tgaggcatat	ttcctagatc	atthttgcctc	tacgatgttt	tttcttggtc	caccttttagg	406
aagggtattga	gaagcaagaa	actggaggcc	caatatctaa	cctgcaaatac	gttttttgagt	466
ttggcaataa	aggctaatac	acccccaaaa	aaa			499

<210> 76
 <211> 978
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> sig_peptide
 <222> 274..399
 <223> Von Heijne matrix




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score 5.19999980926514
seq LLFDLVCHEFCQS/DD
<220>
<221> polyA_signal
<222> 943..948
<220>
<221> polyA_site
<222> 966..978
<220>
<221> misc_feature
<222> 335..518
<223> homology
      id :AA206225
      est
<220>
<221> misc_feature
<222> 225..274
<223> homology
      id :AA206225
      est
<220>
<221> misc_feature
<222> 812..861
<223> homology
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      est
<220>
<221> misc_feature
<222> 186..224
<223> homology
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      est
<220>
<221> misc_feature
<222> 708..748
<223> homology
      id :AA206225
      est
<220>
<221> misc_feature
<222> 276..314
<223> homology
      id :AA206225
      est
<220>
<221> misc_feature
<222> 146..176
<223> homology
      id :AA206225
      est
<220>
<221> misc_feature
<222> 879..909
<223> homology
      id :AA206225
      est
<220>
<221> misc_feature

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230


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<222> 182..518
<223> homology
      id :C15003
      est
<220>
<221> misc_feature
<222> 708..748
<223> homology
      id :C15003
      est
<220>
<221> misc_feature
<222> 182..517
<223> homology
      id :HUM407E11B
      est
<220>
<221> misc_feature
<222> 170..202
<223> homology
      id :AA544037
      est
<220>
<221> misc_feature
<222> 517..595
<223> homology
      id :HUM00TW170
      est
<220>
<221> misc_feature
<222> 596..665
<223> homology
      id :HUM00TW170
      est
<220>
<221> misc_feature
<222> 697..748
<223> homology
      id :HUM00TW170
      est
<220>
<221> misc_feature
<222> 805..861
<223> homology
      id :HUM00TW170
      est
<220>
<221> misc_feature
<222> 212..369
<223> homology
      id :HUM169E08B
      est
<220>
<221> misc_feature
<222> 406..493
<223> homology
      id :HUM169E08B
      est

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<220>
<221> misc_feature
<222> 542..595
<223> homology
      id :HUM00TW112
      est
<220>
<221> misc_feature
<222> 697..748
<223> homology
      id :HUM00TW112
      est
<400> 76
accaggaaca tccagctatt tatgatagca tttgcttcat tatgtcaagt tcaacaaatg      60
ttgacttgct ggtgaagggtg ggggaggttg tggacaagct ctttgatttg gatgagaaac      120
taatgttaag aatgggtcag aaatggggct gctcagcctc tggaccaacc ccaggaagag      180
tctgaagagc agccagtgtt tcggcttggtg ccctgtatac ttgaagctgc caaacaagta      240
cgttctgaaa atccagaatg gcttgatggt tac atg cac att tta caa ctg ctt      294
                               Met His Ile Leu Gln Leu Leu
                               -40
act aca gtg gat gat gga att caa gca att gta cat tgt cct gac act      342
Thr Thr Val Asp Asp Gly Ile Gln Ala Ile Val His Cys Pro Asp Thr
-35                               -30                               -25                               -20
gga aaa gac att tgg aat tta ctt ttt gac ctg gtc tgc cat gaa ttc      390
Gly Lys Asp Ile Trp Asn Leu Leu Phe Asp Leu Val Cys His Glu Phe
                               -15                               -10                               -5
tgc cag tct gat gat cca gcc atc att ctt caa gaa cag aaa aca gtg      438
Cys Gln Ser Asp Asp Pro Ala Ile Ile Leu Gln Glu Gln Lys Thr Val
                               1                               5                               10
cta gcc tct gtt ttt tca gtg ttg tct gcc atc tat gcc tca cag act      486
Leu Ala Ser Val Phe Ser Val Leu Ser Ala Ile Tyr Ala Ser Gln Thr
                               15                               20                               25
gag caa gag tat cta aag ata gaa aaa gta gat ctt cct cta att gac      534
Glu Gln Glu Tyr Leu Lys Ile Glu Lys Val Asp Leu Pro Leu Ile Asp
30                               35                               40                               45
agc ctc att cgg gtc tta caa aat atg gaa cag tgt cag aaa aaa cca      582
Ser Leu Ile Arg Val Leu Gln Asn Met Glu Gln Cys Gln Lys Lys Pro
                               50                               55                               60
gag aac tcg gca gga gtc taacacagag gaaactaaaa ggactgattt      630
Glu Asn Ser Ala Gly Val
                               65
aacc caagat gatttccact tgaaaatctt aaaaggatat tggttatggtg aagtttctgt      690
ctaataattt ttcaggcatt aacaaaggag acggtggctc agggagtaaa ggaaggccgt      750
tgagcaaaca gaagtgttcc tctgcaattt caaaarcctt cttctttcta tagccctgt      810
gggtggaaga ttttattaaa atcctacgtg aagttgataa ggcgcttgct kgatgacttg      870
gaaaaaaamc ttccaagtt tgaaggttca gaastaaaaa rscktgaatg ggaattactt      930
sstgtbcaag aaaataaact ttatttttct cactgaaaaa aaaaaaaa      978

<210> 77
<211> 587
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 421..465
<223> Von Heijne matrix
      score 3.90000009536743
      seq LVPLGQSFPLSEP/RC

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<220>
<221> polyA_signal
<222> 553..558
<220>
<221> polyA_site
<222> 575..587
<220>
<221> misc_feature
<222> 182..322
<223> homology
      id :T35951
      est
<220>
<221> misc_feature
<222> 32..132
<223> homology
      id :T35951
      est
<220>
<221> misc_feature
<222> 136..193
<223> homology
      id :T35951
      est
<220>
<221> misc_feature
<222> 182..322
<223> homology
      id :T35949
      est
<220>
<221> misc_feature
<222> 32..132
<223> homology
      id :T35949
      est
<220>
<221> misc_feature
<222> 136..193
<223> homology
      id :T35949
      est
<220>
<221> misc_feature
<222> 136..299
<223> homology
      id :AA381111
      est
<220>
<221> misc_feature
<222> 32..132
<223> homology
      id :AA381111
      est
<220>
<221> misc_feature
<222> 136..322
<223> homology

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233


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        id :AA381001
        est
<220>
<221> misc_feature
<222> 85..132
<223> homology
        id :AA381001
        est
<220>
<221> misc_feature
<222> 182..322
<223> homology
        id :HSCZQE041
        est
<220>
<221> misc_feature
<222> 136..193
<223> homology
        id :HSCZQE041
        est
<220>
<221> misc_feature
<222> 82..132
<223> homology
        id :HSCZQE041
        est
<220>
<221> misc_feature
<222> 316..428
<223> homology
        id :AA477628
        est
<220>
<221> misc_feature
<222> 475..554
<223> homology
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        est
<220>
<221> misc_feature
<222> 182..322
<223> homology
        id :HSC34G011
        est
<220>
<221> misc_feature
<222> 136..192
<223> homology
        id :HSC34G011
        est
<220>
<221> misc_feature
<222> 41..119
<223> homology
        id :AA090647
        est
<220>
<221> misc_feature

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<222> 136..184
<223> homology
      id :AA090647
      est
<220>
<221> misc_feature
<222> 316..426
<223> homology
      id :AA505962
      est
<400> 77
aattcattttt tcactcctcc ctccctagggtc acactttttca gaaaaagaat ctgcatactg      60
gaaaccagaa gaaaaatatg agacgggggaa tcatcgtgtg atgtgtgtgc tgcctttggc      120
tkwgtgtgk gaagtycckg ctccaggtgtt aggtacagtg tgtttgatcg tgggtggctg      180
aggggaaccc gctgttcaga gctgtgactg cggctgcact cagagaagct gcccttggt      240
gctcgtagcg ccgggccttc tctcctcgtc atcatccaga gcagccagt tccgggaggg      300
agaagatgcc ccactccagc ctctggactg ggggctctct tcagtggctg aatgtccagc      360
agagctattt ccttccacag ggggccttgc aggggaagggt ccaggacttg acatcttaag      420
atg cgt ctt gtc ccc ttg ggc cag tca ttt ccc ctc tct gag cct cgg      468
Met Arg Leu Val Pro Leu Gly Gln Ser Phe Pro Leu Ser Glu Pro Arg
-15 -10 -5 1
tgt ctt caa cct gtg aaa tgg gat cat aat cac tgc ctt acc tcc ctc      516
Cys Leu Gln Pro Val Lys Trp Asp His Asn His Cys Leu Thr Ser Leu
5 10 15
acg gtt gtt gtg agg act gag tgt gtg gaa gtt ttt cat aaa ctt tgg      564
Thr Val Val Val Arg Thr Glu Cys Val Glu Val Phe His Lys Leu Trp
20 25 30
atg cta gtg taaaaaaaaa aaaa      587
Met Leu Val
35

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<210> 78
<211> 400
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 198..278
<223> Von Heijne matrix
      score 4.90000009536743
      seq CLLSYIALGAIHA/KI
<220>
<221> polyA_signal
<222> 364..369
<220>
<221> polyA_site
<222> 387..400
<400> 78
aactttgcct ggggtgtcttg cgttctgcac attccggagg accagcttcc ccatcagaag      60
tctgactcca tggaaaccag atggggcaac ggggtggttc tagtgcagac tgtagctgca      120
gctcctctcc acctctagcc tgctcatttc cagctcagaa attctactaa tggcgttttt      180
tcttcctgaa aaaggaa atg aac agg gtc cct gct gat tct cca aat atg      230
      Met Asn Arg Val Pro Ala Asp Ser Pro Asn Met
      -25 -20
tgt cta atc tgt tta ctg agt tac ata gca ctt gga gcc atc cat gca      278
Cys Leu Ile Cys Leu Leu Ser Tyr Ile Ala Leu Gly Ala Ile His Ala
-15 -10 -5
aaa atc tgt aga aga gca ttc cag gaa gag gga aga gca aat gca aag      326

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235

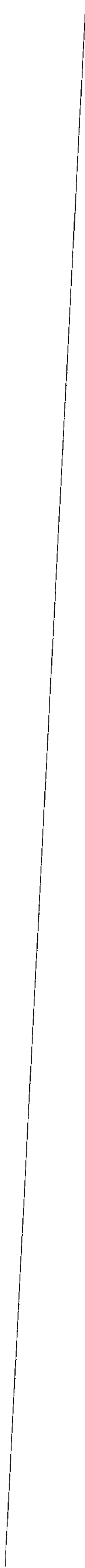
Lys	Ile	Cys	Arg	Arg	Ala	Phe	Gln	Glu	Glu	Gly	Arg	Ala	Asn	Ala	Lys	
1				5				10					15			
acg	ggc	gtg	aga	gct	tgg	tgc	ata	cag	cca	tgg	gcc	aaa	taa	agtttcc		375
Thr	Gly	Val	Arg	Ala	Trp	Cys	Ile	Gln	Pro	Trp	Ala	Lys				
			20				25									
ttggaatagc	caaaaaaaaaa	aaaaa														400

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<210> 79
<211> 1166
<212> DNA
<213> Homo sapiens
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      score 5.59999990463257
      seq LVLSLQFLLLSYD/LF
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<221> polyA_signal
<222> 1133..1138
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<221> polyA_site
<222> 1154..1166
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<221> misc_feature
<222> 22..377
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      est
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<222> 424..540
<223> homology
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<220>
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      est
<220>
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<223> homology
      id :AA417777
      est
<220>
<221> misc_feature
<222> 10..447
<223> homology
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<220>
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<222> 279..714
<223> homology
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236



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        est
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<223> homology
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<220>
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<222> 1056..1109
<223> homology
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<222> 1122..1153
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<222> 1024..1054

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ttcaaaggaa ctagaagcct ctccctcagt ggtagggaga cagccaggag cggttttctg      120
ggaactgtgg gatgtgccct tgggggcccg agaaaacaga aggaag atg ctc cag      175
                                         Met Leu Gln
                                         -20
acc agt aac tac agc ctg gtg ctc tct ctg cag ttc ctg ctg ctg tcc      223
Thr Ser Asn Tyr Ser Leu Val Leu Ser Leu Gln Phe Leu Leu Leu Ser
      -15                               -10                               -5
tat gac ctc ttt gtc aat tcc ttc tca gaa ctg ctc caa aag act cct      271
Tyr Asp Leu Phe Val Asn Ser Phe Ser Glu Leu Leu Gln Lys Thr Pro
      1                               5                               10
gtc atc cag ctt gtg ctc ttc atc atc cag gat att gca gtc ctc ttc      319
Val Ile Gln Leu Val Leu Phe Ile Ile Gln Asp Ile Ala Val Leu Phe
15                               20                               25                               30
aac atc atc atc att ttc ctc atg ttc ttc aac acc tcc gtc ttc cag      367
Asn Ile Ile Ile Ile Phe Leu Met Phe Phe Asn Thr Ser Val Phe Gln
      35                               40                               45
gct ggc ctg gtc aac ctc cta ttc cat aag ttc aaa ggg acc atc atc      415
Ala Gly Leu Val Asn Leu Leu Phe His Lys Phe Lys Gly Thr Ile Ile
      50                               55                               60
ctg aca gct gtg tac ttt gcc ctc agc atc tcc ctt cat gtc tgg gtc      463
Leu Thr Ala Val Tyr Phe Ala Leu Ser Ile Ser Leu His Val Trp Val
      65                               70                               75
atg aac tta cgc tgg aaa aac tcc aac agc ttc ata tgg aca gat gga      511
Met Asn Leu Arg Trp Lys Asn Ser Asn Ser Phe Ile Trp Thr Asp Gly
      80                               85                               90

```


ctt	caa	atg	ctg	ttt	gta	ttc	cag	aga	cta	gca	gca	gtg	ttg	tac	tgc	559
Leu	Gln	Met	Leu	Phe	Val	Phe	Gln	Arg	Leu	Ala	Ala	Val	Leu	Tyr	Cys	
95					100					105					110	
tac	ttc	tat	aaa	cgg	aca	gcc	gta	aga	cta	ggc	gat	cct	cac	ttc	tac	607
Tyr	Phe	Tyr	Lys	Arg	Thr	Ala	Val	Arg	Leu	Gly	Asp	Pro	His	Phe	Tyr	
			115						120					125		
cag	gac	tct	ttg	tgg	ctg	cgc	aag	gag	ttc	atg	caa	gtt	cga	agg		652
Gln	Asp	Ser	Leu	Trp	Leu	Arg	Lys	Glu	Phe	Met	Gln	Val	Arg	Arg		
			130					135					140			
tgacctcttg	tcacactgat	ggatactttt	ccttctctgat	agaagccaca	tttgctgctt											712
tgcagggaga	gttggcccta	tgcattgggca	aacagctgga	ctttccaagg	aagggttcaga											772
ctagctgtgt	tcagcattca	agaaggaaga	tccccctct	tgcacaatta	gagtgtcccc											832
atcggctctcc	agtgcggcat	cccttctctg	ccttctacct	ctgttccacc	cccttctctc											892
ctctcctctc	tgtaccattc	attctccctg	accggccttt	cttgccgagg	gttctgtggc											952
tcttaccctt	gtgaagcttt	tccttttagcc	tgggacagaa	ggacctcccg	gcccccaaag											1012
gatctcccag	wtgaccaaag	gatgcgaaga	gtgatagtta	cgntgctcct	gactgatcac											1072
accgcagaca	tttagatttt	tatacccaag	gcacttttaa	aaaatgtttt	ataaatagag											1132
aataaattga	attyttgttc	caaaaaaaaa	aaaa													1166

<210> 80
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 <223> Von Heijne matrix
 score 4.59999990463257
 seq LPFSLVSMMLVTQG/LV
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 <221> polyA_signal
 <222> 722..727
 <220>
 <221> polyA_site
 <222> 743..754
 <220>
 <221> misc_feature
 <222> 116..450
 <223> homology
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 <220>
 <221> misc_feature
 <222> 593..710
 <223> homology
 id :W68799
 est
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 <222> 18..117
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 est
 <220>
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 <222> 561..598
 <223> homology
 id :W68799

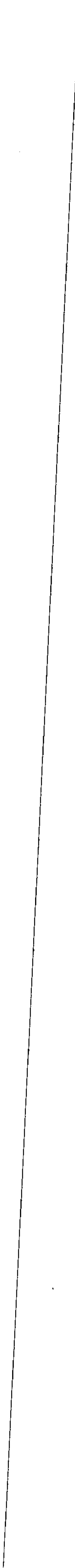
239


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      est
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<222> 48..511
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      est
<220>
<221> misc_feature
<222> 535..710.
<223> homology
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<220>
<221> misc_feature
<222> 256..405
<223> homology
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      est
<220>
<221> misc_feature
<222> 432..511
<223> homology
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      est
<220>
<221> misc_feature
<222> 392..437
<223> homology
      id :W80356
      est
<220>
<221> misc_feature
<222> 535..710
<223> homology
      id :W80631
      est
<220>
<221> misc_feature
<222> 289..437
<223> homology
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<221> misc_feature
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      est
<220>
<221> misc_feature
<222> 343..511

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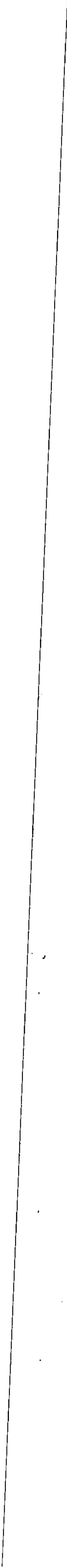


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<223> homology
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<220>
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<222> 256..341
<223> homology
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      est
<220>
<221> misc_feature
<222> 248..511
<223> homology
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<220>
<221> misc_feature
<222> 21..271
<223> homology
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<220>
<221> misc_feature
<222> 121..450
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<220>
<221> misc_feature
<222> 592..710
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      est
<220>
<221> misc_feature
<222> 725
<223> n=a, g, c or t
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ggcctgctgg gcttggcaac gagggactcg gcctcggagg cgacccagac cacacagaca      120
ctgggtcaag gagtaagcag aggataaaca actggaagga gagcaagcac aaagtcac      179
atg gct tca gcg tct gct cgt gga aac caa gat aaa gat gcc cat ttt      227
Met Ala Ser Ala Ser Ala Arg Gly Asn Gln Asp Lys Asp Ala His Phe
      -65                      -60                      -55
cca cca cca agc aag cag agc ctg ttg ttt tgt cca aaa tca aaa ctg      275
Pro Pro Pro Ser Lys Gln Ser Leu Leu Phe Cys Pro Lys Ser Lys Leu
      -50                      -45                      -40
cac atc cac aga gca gag atc tca aag att atg cga gaa tgt cag gaa      323
His Ile His Arg Ala Glu Ile Ser Lys Ile Met Arg Glu Cys Gln Glu
      -35                      -30                      -25
gaa agt ttc tgg aag aga gct ctg cct ttt tct ctt gta agc atg ctt      371
Glu Ser Phe Trp Lys Arg Ala Leu Pro Phe Ser Leu Val Ser Met Leu

```

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10/20/2019

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10/20/2019

-20		-15		-10		-5	
gtc acc cag gga cta gtc tac caa ggt tat ttg gca gct aat tct aga							419
Val Thr Gln Gly Leu Val Tyr Gln Gly Tyr Leu Ala Ala Asn Ser Arg							
	1		5		10		
ttt gga tca ttg ccc aaa gtt gca ctt gct ggt ctc ttg gga ttt ggc							467
Phe Gly Ser Leu Pro Lys Val Ala Leu Ala Gly Leu Leu Gly Phe Gly							
	15		20		25		
ctt gga aag gta tca tac ata gga gta tgc cag agt aaa ttc cat ttt							515
Leu Gly Lys Val Ser Tyr Ile Gly Val Cys Gln Ser Lys Phe His Phe							
	30		35		40		
ttt gaa gat cag ctc cgt ggg gct ggt ttt ggt ccw aca gca							557
Phe Glu Asp Gln Leu Arg Gly Ala Gly Phe Gly Pro Thr Ala							
	45		50		55		
taacagggcac tgcctcctta cctgtgagga atgcaaaata aagcatggat taagtgagaa							617
gggagactct cagccttcag cttcctaaat tctgtgtctg tgactttcga agttttttaa							677
acctctgaat ttgtacacat ttaaaatttc aaggtgtact ttaaaatnaa aatacttcta							737
atgtvaaaaa aaaaaaa							754

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<210> 81
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<221> sig_peptide
<222> 179..298
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      seq ITLVSAAPGKVIC/EM
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<221> polyA_signal
<222> 680..685
<220>
<221> polyA_site
<222> 697..708
<220>
<221> misc_feature
<222> 137..291
<223> homology
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      est
<220>
<221> misc_feature
<222> 6..91
<223> homology
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      est
<220>
<221> misc_feature
<222> 318..397
<223> homology
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      est
<220>
<221> misc_feature
<222> 95..132
<223> homology
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      est

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242


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<220>
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<222> 460..501
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<220>
<221> misc_feature
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<223> homology
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      est

<220>
<221> misc_feature
<222> 284..313
<223> homology
      id :AA121372
      est

<220>
<221> misc_feature
<222> 254..670
<223> homology
      id :AA614605
      est

<220>
<221> misc_feature
<222> 392..658
<223> homology
      id :T55234
      est

<220>
<221> misc_feature
<222> 271..327
<223> homology
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      est

<220>
<221> misc_feature
<222> 358..670
<223> homology
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      est

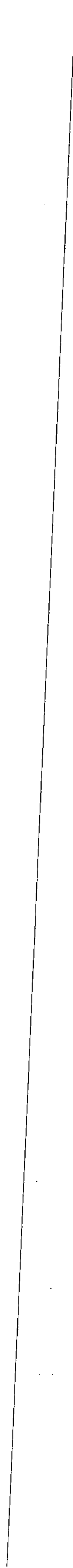
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<222> 312..344
<223> homology
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      est

<220>
<221> misc_feature
<222> 2..102
<223> homology
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      est

<220>
<221> misc_feature
<222> 150..258
<223> homology

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        id :T53974
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<220>
<221> misc_feature
<222> 95..171
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<220>
<221> misc_feature
<222> 322..628
<223> homology
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        est
<220>
<221> misc_feature
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<223> homology
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<220>
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        est
<220>
<221> misc_feature
<222> 95..171
<223> homology
        id :R09314
        est
<220>
<221> misc_feature
<222> 150..222
<223> homology
        id :R09314
        est
<400> 81
aaaatcgcg accaccggg ctgccakctc gcctgactcc cggcctcttg cgctcctagg      60
ggcggagaag ggtgcgggct ctgcgccctt tgtgtccttc ttccactaac ttctggactt      120
tccagctctt ccgaagtctg ttcttgcgca aagcccaaag gctggaaaac cgtccacg      178
atg acc agc atg act cag tct ctg cgg gag gtg ata aag gcc atg acc      226
Met Thr Ser Met Thr Gln Ser Leu Arg Glu Val Ile Lys Ala Met Thr
-40                               -35                               -30                               -25
aag gct cgc aat ttt gag aga gtt ttg gga aag att act ctt gtc tct      274
Lys Ala Arg Asn Phe Glu Arg Val Leu Gly Lys Ile Thr Leu Val Ser
-20                               -15                               -10
gct gct cct ggg aaa gtg att tgt gaa atg aaa gta gaa gaa gag cat      322
Ala Ala Pro Gly Lys Val Ile Cys Glu Met Lys Val Glu Glu Glu His
-5                               1                               5
acc aat gca ata ggc act ctc cac ggc ggt ttg aca gcc acg tta gta      370
Thr Asn Ala Ile Gly Thr Leu His Gly Gly Leu Thr Ala Thr Leu Val
10                               15                               20
gat aac ata tca aca atg gct ctg cta tgc acg gaa agg gga gca ccc      418
Asp Asn Ile Ser Thr Met Ala Leu Leu Cys Thr Glu Arg Gly Ala Pro
25                               30                               35                               40
gga gtc agt gtc gat atg aac ata acg tac atg tca cct gca aaa tta      466

```

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2020

Gly	Val	Ser	Val	Asp	Met	Asn	Ile	Thr	Tyr	Met	Ser	Pro	Ala	Lys	Leu	
				45				50						55		
gga	gag	gat	ata	gtg	att	aca	gca	cat	gtt	ctg	aag	caa	gga	aaa	aca	514
Gly	Glu	Asp	Ile	Val	Ile	Thr	Ala	His	Val	Leu	Lys	Gln	Gly	Lys	Thr	
			60					65					70			
ctt	gca	ttt	acc	tct	gtg	ggt	ctg	acc	aac	aag	gcc	aca	gga	aaa	tta	562
Leu	Ala	Phe	Thr	Ser	Val	Gly	Leu	Thr	Asn	Lys	Ala	Thr	Gly	Lys	Leu	
		75					80					85				
ata	gca	caa	gga	aga	cac	aca	aaa	cac	ctg	gga	aac	tgagagaaca				608
Ile	Ala	Gln	Gly	Arg	His	Thr	Lys	His	Leu	Gly	Asn					
	90					95				100						
gcagaatgac	ctaaagaaac	ccaacaatga	atatcaagta	tagatttgac	tcaaacaatt											668
gtaattttttg	aaataaacta	gcaaaaccaa	aaaaaaaaaa	g												709

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<210> 82
<211> 243
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 100..171
<223> Von Heijne matrix
      score 3.70000004768372
      seq ILFNLLIFLCGFT/NY
<220>
<221> polyA_signal
<222> 211..216
<220>
<221> polyA_site
<222> 230..243
<220>
<221> misc_feature
<222> 2..164
<223> homology
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      est
<220>
<221> misc_feature
<222> 2..164
<223> homology
      id :AA131065
      est
<220>
<221> misc_feature
<222> 5..164
<223> homology
      id :AA224847
      est
<220>
<221> misc_feature
<222> 10..164
<223> homology
      id :AA161042
      est
<220>
<221> misc_feature
<222> 2..84
<223> homology

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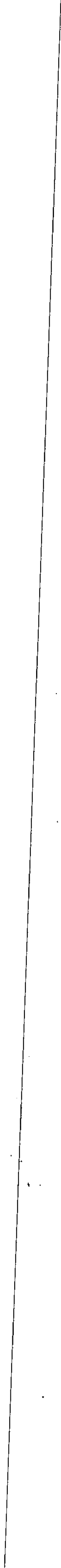
245


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<221> misc_feature
<222> 10..164
<223> homology
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<221> misc_feature
<222> 79..164
<223> homology
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<223> homology
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<220>
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<221> misc_feature
<222> 158..207
<223> homology
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<223> homology
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        est
<220>
<221> misc_feature

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<222> 160..207
<223> homology
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<220>
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<220>
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      est

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<220>
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<220>
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<222> 200..229
<223> homology
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aactcagtgg caacacccgg gagctgtttt gtcctttgtg gagcctcagc agttccctct      60
ttcagaactc actgccaaga gccctgaaca ggagccacc atg cag tgc ttc agc      114
                                   Met Gln Cys Phe Ser
                                   -20
ttc att aag acc atg atg atc ctc ttc aat ttg ctc atc ttt ctg tgt      162
Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu Leu Ile Phe Leu Cys
                                   -15      -10      -5
ggc ttc acc aac tat acg gat ttt gag gac tca ccc tac ttc aaa atg      210
Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp Ser Pro Tyr Phe Lys Met
                                   1      5      10
cat aaa cct gtt aca atg taaaaaaaaa aaaaaa      243
His Lys Pro Val Thr Met
      15

<210> 83
<211> 829
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 346..408
<223> Von Heijne matrix
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seq SFLPSALVIWTSA/AF
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<221> polyA_signal
<222> 792..797
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<221> polyA_site
<222> 817..829
<220>
<221> misc_feature
<222> 260..464
<223> homology
      id :H57434
      est
<220>
<221> misc_feature
<222> 118..184
<223> homology
      id :H57434
      est
<220>
<221> misc_feature
<222> 56..113
<223> homology
      id :H57434
      est
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<222> 454..485
<223> homology
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      est
<220>
<221> misc_feature
<222> 118..545
<223> homology
      id :N27248
      est
<220>
<221> misc_feature
<222> 65..369
<223> homology
      id :H94779
      est
<220>
<221> misc_feature
<222> 471..519
<223> homology
      id :H94779
      est
<220>
<221> misc_feature
<222> 61..399
<223> homology
      id :H09880
      est
<220>
<221> misc_feature
<222> 408..452

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248


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<223> homology
      id :H09880
      est
<220>
<221> misc_feature
<222> 60..399
<223> homology
      id :H29351
      est
<220>
<221> misc_feature
<222> 393..432
<223> homology
      id :H29351
      est
<220>
<221> misc_feature
<222> 260..444
<223> homology
      id :AA459511
      est
<220>
<221> misc_feature
<222> 449..545
<223> homology
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      est
<220>
<221> misc_feature
<222> 117..184
<223> homology
      id :AA459511
      est
<220>
<221> misc_feature
<222> 122..399
<223> homology
      id :T74091
      est
<220>
<221> misc_feature
<222> 393..434
<223> homology
      id :T74091
      est
<220>
<221> misc_feature
<222> 61..378
<223> homology
      id :HSC3CB081
      est
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<221> misc_feature
<222> 118..399
<223> homology
      id :T82010
      est
<220>

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249


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<221> misc_feature
<222> 268..545
<223> homology
      id :W02860
      est
<220>
<221> misc_feature
<222> 268..545
<223> homology
      id :N44490
      est
<220>
<221> misc_feature
<222> 115
<223> n=a, g, c or t
<400> 83
actccttttta gcataggggc ttcggcgcca gcggccagcg ctagtcgggc tggtaagtgc      60
ctgatgccga gttccgtctc tcgcgtcttt tcctgggtccc aggcaaagcg gasgnagatc      120
ctcaaacggc ctagtgcttc gcgcttccgg agaaaatcag cggctctaatt aattcctctg      180
gtttgttgaa gcagttacca agaattctca accctttccc acaaaagcta attgagtaca      240
cgttcctgtt gagtacacgt tcctgttgat ttacaaaagg tgcaggtatg agcaggtctg      300
aagactaaca ttttgtgaag ttgtaaaaca gaaaacctgt tagaa atg tgg tgg ttt      357
                                   Met Trp Trp Phe
                                   -20
cag caa ggc ctc agt ttc ctt cct tca gcc ctt gta att tgg aca tct      405
Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val Ile Trp Thr Ser
      -15                               -10                               -5
gct gct ttc ata ttt tca tac att act gca gta aca ctc cac cat ata      453
Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr Leu His His Ile
      1                               5                               10                               15
gac ccg gct tta cct tat atc agt gac act ggt aca gta gct cca gaa      501
Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr Val Ala Pro Glu
      20                               25                               30
aaa tgc tta ttt ggg gca atg cta aat att gcg gca gtc tta tgt caa      549
Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala Val Leu Cys Gln
      35                               40                               45
aaa tagaaatcag gaagataatt caacttaaag aagttcattt catgaccaa      602
Lys
ctcttcagaa acatgtcttt acaagcatat ctcttgtatt gctttctaca ctgttgaatt      662
gtctggcaat atttctgcag tggaaaattt gatttagcta gttcttgact tggataaata      722
tggttaaggtg ggcttttccc cctgtgtaat tggctacsac gtcttacttg agccaagttg      782
gtaagttgaa ataaaatgat watgagagtg acacavaaaa aaaaaaa      829

<210> 84
<211> 674
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 177..233
<223> Von Heijne matrix
      score 6.09999990463257
      seq LALLWSLPASDLG/RS
<220>
<221> polyA_signal
<222> 644..649
<220>
<221> polyA_site

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<222> 663..674
<220>
<221> misc_feature
<222> 194..592
<223> homology
      id :AA496246
      est
<220>
<221> misc_feature
<222> 1..100
<223> homology
      id :AA496246
      est
<220>
<221> misc_feature
<222> 99..202
<223> homology
      id :AA496246
      est
<220>
<221> misc_feature
<222> 187..592
<223> homology
      id :AA476481
      est
<220>
<221> misc_feature
<222> 594..661
<223> homology
      id :AA476481
      est
<220>
<221> misc_feature
<222> 188..592
<223> homology
      id :AA496245
      est
<220>
<221> misc_feature
<222> 594..661
<223> homology
      id :AA496245
      est
<220>
<221> misc_feature
<222> 194..444
<223> homology
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      est
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<222> 1..102
<223> homology
      id :AA476480
      est
<220>
<221> misc_feature
<222> 99..187

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251

<223> homology
id :AA476480
est

<220>

<221> misc_feature

<222> 437..592

<223> homology

id :AA505488

est

<220>

<221> misc_feature

<222> 594..661

<223> homology

id :AA505488

est

<220>

<221> misc_feature

<222> 441..592

<223> homology

id :AA554685

est

<220>

<221> misc_feature

<222> 594..661

<223> homology

id :AA554685

est

<220>

<221> misc_feature

<222> 414..503

<223> homology

id :AA215595

est

<220>

<221> misc_feature

<222> 510..539

<223> homology

id :AA215595

est

<400> 84

ataagtgaac cagaccaccc tgatggcatc cacagtgatg tcaagggttg ggctggccag 60

gggtgggttg actagaagca tttgggagta gtggccagg ggcctggacg ctagccacgg 120

agctgctgca cagagcctgg tgtccacaag cttccagggtt ggggttgagg cctggg atg 179

Met

agc ccc ggc agc gcc ttg gcc ctt ctg tgg tcc ctg cca gcc tct gac 227

Ser Pro Gly Ser Ala Leu Ala Leu Leu Trp Ser Leu Pro Ala Ser Asp

-15

-10

-5

ctg ggc cgg tca gtc att gct gga ctc tgg cca cac act ggc gtt ctc 275

Leu Gly Arg Ser Val Ile Ala Gly Leu Trp Pro His Thr Gly Val Leu

1

5

10

atc cac ttg gaa aca agc cag tct ttt ctg caa ggt cag ttg acc aag 323

Ile His Leu Glu Thr Ser Gln Ser Phe Leu Gln Gly Gln Leu Thr Lys

15

20

25

30

agc ata ttt ccc ctc tgt tgt aca tcg ttg ttt tgt gtt tgt gtt gta 371

Ser Ile Phe Pro Leu Cys Cys Thr Ser Leu Phe Cys Val Cys Val Val

35

40

45

aca gtg ggt gga ggg agg gtg ggg tct aca ttt gtt gca tgagtcgatg 420

Thr Val Gly Gly Gly Arg Val Gly Ser Thr Phe Val Ala

252

	50	55	
ggtcagaact	ttagtatacg	catgcgtcct	ctgagtgaca gggcattttg tcgaaaataa 480
gcaccttggt	aactaaaccc	ctctaatagc	tataaaggct ttagttctgt attgattaag 540
ttactgtaaa	agcttgggtt	tatttttgta	ggacttaatg gctaagaatt agggaacata 600
gcaagggggc	tcctctgttg	gagtaatgta	aattgtaatt ataaataaac atgcaaacct 660
ttaaaaaaaa	aaaa		674

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<210> 85
<211> 478
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 179..319
<223> Von Heijne matrix
      score 5.5
      seq SALLFFARPCVFC/FK
<220>
<221> polyA_signal
<222> 461..466
<220>
<221> polyA_site
<222> 465..478
<220>
<221> misc_feature
<222> 2..464
<223> homology
      id :AA310996
      est
<220>
<221> misc_feature
<222> 8..464
<223> homology
      id :AA312901
      est
<220>
<221> misc_feature
<222> 2..416
<223> homology
      id :AA401411
      est
<220>
<221> misc_feature
<222> 2..349
<223> homology
      id :R64030
      est
<220>
<221> misc_feature
<222> 56..464
<223> homology
      id :AA400108
      est
<220>
<221> misc_feature
<222> 126..273
<223> homology
      id :AA010825

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253


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        est
<220>
<221> misc_feature
<222> 2..147
<223> homology
        id :AA010825
        est
<220>
<221> misc_feature
<222> 358..435
<223> homology
        id :AA010825
        est
<220>
<221> misc_feature
<222> 78..464
<223> homology
        id :AA504732
        est
<220>
<221> misc_feature
<222> 90..441
<223> homology
        id :H60506
        est
<220>
<221> misc_feature
<222> 59..349
<223> homology
        id :AA346780
        est
<220>
<221> misc_feature
<222> 2..331
<223> homology
        id :AA281167
        est
<220>
<221> misc_feature
<222> 6..236
<223> homology
        id :R35805
        est
<220>
<221> misc_feature
<222> 232..284
<223> homology
        id :R35805
        est
<220>
<221> misc_feature
<222> 41..307
<223> homology
        id :H13784
        est
<220>
<221> misc_feature
<222> 2..40

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254


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<223> homology
      id :H13784
      est
<220>
<221> misc_feature
<222> 64..280
<223> homology
      id :AA128122
      est
<220>
<221> misc_feature
<222> 293..349
<223> homology
      id :AA128122
      est
<220>
<221> misc_feature
<222> 332..385
<223> homology
      id :AA128122
      est
<220>
<221> misc_feature
<222> 163..420
<223> homology
      id :AA555127
      est
<400> 85
aagtccttcg cgccctcctc gccctcccca ccgacatcat gctccagttc ctgcttggat      60
ttacactggg caacgtgggt ggaatgtatc tggctcagaa ctatgatata ccaaacctgg      120
ctaaaaaact tgaagaaatt aaaaaggact tggatgccaa gaagaaaccc cctagtgc      178
atg aga ctg cct cca gca ctg cct tca gga tat act gat tct act gct      226
Met Arg Leu Pro Pro Ala Leu Pro Ser Gly Tyr Thr Asp Ser Thr Ala
      -45                      -40                      -35
ctt gag ggc ctc gtt tac tat ctg aac caa aag ctt ttg ttt tcg tct      274
Leu Glu Gly Leu Val Tyr Tyr Leu Asn Gln Lys Leu Leu Phe Ser Ser
      -30                      -25                      -20
cca gcc tca gca ctt ctc ttc ttt gct aga ccc tgt gtt ttt tgc ttt      322
Pro Ala Ser Ala Leu Leu Phe Phe Ala Arg Pro Cys Val Phe Cys Phe
      -15                      -10                      -5                      1
aaa gca agc aaa atg ggg ccc caa ttt gag aac tac cca aca ttt cca      370
Lys Ala Ser Lys Met Gly Pro Gln Phe Glu Asn Tyr Pro Thr Phe Pro
      5                      10                      15
aca tac tca cct ctt ccc ata atc cct ttc caa ctg cat ggg agg ttc      418
Thr Tyr Ser Pro Leu Pro Ile Ile Pro Phe Gln Leu His Gly Arg Phe
      20                      25                      30
taagactgga attatggtgc tagattagta aacatgactt ttaatgaaaa aaaaacaaaa      478

<210> 86
<211> 952
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 112..237
<223> Von Heijne matrix
      score 7.19999980926514
      seq ILFSLSFLLVIIT/FP

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255



12

12

12

12

12

12

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12

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12

12


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<220>
<221> polyA_signal
<222> 910..915
<220>
<221> polyA_site
<222> 940..952
<400> 86
aatacttttct cctctcccct ctcccaagca catctgagtt gctgcctggt cttcacactt      60
agctccaaac ccataaaaaa ttgccaagta taaaagcttc tcaagaatga g atg gat      117
                               Met Asp
tct agg gtg tct tca cct gag aag caa gat aaa gag aat ttc gtg ggt      165
Ser Arg Val Ser Ser Pro Glu Lys Gln Asp Lys Glu Asn Phe Val Gly
-40                               -35                               -30                               -25
gtc aac aat aaa cgg ctt ggt gta tgt ggc tgg atc ctg ttt tcc ctc      213
Val Asn Asn Lys Arg Leu Gly Val Cys Gly Trp Ile Leu Phe Ser Leu
                               -20                               -15                               -10
tct ttc ctg ttg gtg atc att acc ttc ccc atc tcc ata tgg atg tgc      261
Ser Phe Leu Leu Val Ile Ile Thr Phe Pro Ile Ser Ile Trp Met Cys
                               -5                               1                               5
ttg aag att tgatcctggt cctgccatgc ataratgtgt ttgtcaaagt      310
Leu Lys Ile
10
tgacctccga acagttactt gcaacattcc tccacaagag atcctcacca rgagactccg      370
taactactca ggtagatgga gttgtctatt acagaatcta tagtgctgtc tcagcagtgg      430
ctaakgtcaa cgatgtccat caagcaacat ttctgctggc tcaaaccact ctgagaaatg      490
tcktagggac acaggacctt gtccccagat cttaggctgg acgagaagag atcgcccata      550
agcatccaga ctktacttga tgatgccacc gaactggtgg gggatccggg tggcccgagt      610
ggaaatcaaa gatgttcgga ttcccgtgca gttgcagaga tccatggcag ccgaggstga      670
ggccaccgga gaagsgagag ccaagggtcct tgcagctgaa ggagaaatga atgsttccaa      730
atccctgaag tcagcctcca tgggtgstggs tgagtytccc atagctytcc agstgsgsta      790
cctgcagacc ttgagcacgg tagccaccga gaagaatttt acgattgtgt ttcctbtgcc      850
catgaatata ctagagggca ttggtggcgt cagstatgat aaccacaaga agsttbscaa      910
ataaagcctg aggtcybctt gcggtagtca aaaaaaaaaa aa      952

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<210> 87
<211> 131
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -13..-1
<400> 87
Met Leu Ala Val Ser Leu Thr Val Pro Leu Leu Gly Ala Met Met Leu
                               -10                               -5                               1
Leu Glu Ser Pro Ile Asp Pro Gln Pro Leu Ser Phe Lys Glu Pro Pro
5                               10                               15
Leu Leu Leu Gly Val Leu His Pro Asn Thr Lys Leu Arg Gln Ala Glu
20                               25                               30                               35
Arg Leu Phe Glu Asn Gln Leu Val Gly Pro Glu Ser Ile Ala His Ile
                               40                               45                               50
Gly Asp Val Met Phe Thr Gly Thr Ala Asp Gly Arg Val Val Lys Leu
55                               60                               65
Glu Asn Gly Glu Ile Glu Thr Ile Ala Arg Phe Gly Ser Gly Pro Cys
70                               75                               80
Lys Thr Arg Gly Asp Glu Pro Val Cys Gly Arg Pro Leu Gly Ile Arg
85                               90                               95
Gly Arg Ala Gln Trp Asp Ser Leu Cys Gly Arg Cys Ile Gln Arg Asp
100                               105                               110                               115

```

256



3.1.1.1

3.1.1.2

3.1.1.3

3.1.1.4

3.1.1.5

3.1.1.6

3.1.1.7

3.1.1.8

3.1.1.9

3.1.1.10

3.1.1.11

3.1.1.12

3.1.1.13

3.1.1.14

3.1.1.15

3.1.1.16

3.1.1.17

3.1.1.18

3.1.1.19

3.1.1.20

3.1.1.21

3.1.1.22

3.1.1.23

3.1.1.24

3.1.1.25

3.1.1.26

3.1.1.27

3.1.1.28

3.1.1.29

3.1.1.30

Tyr Leu Lys

<210> 88
<211> 63
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -35...-1
<400> 88

Met	Leu	Thr	Val	Asn	Asp	Val	Arg	Phe	Tyr	Arg	Asn	Val	Arg	Ser	Asn
-35					-30					-25					-20
His	Phe	Pro	Phe	Val	Arg	Leu	Cys	Gly	Leu	Leu	His	Leu	Trp	Leu	Lys
				-15					-10					-5	
Val	Phe	Ser	Leu	Lys	Gln	Leu	Lys	Lys	Lys	Ser	Trp	Ser	Lys	Tyr	Leu
			1				5					10			
Phe	Glu	Ser	Cys	Cys	Tyr	Arg	Ser	Leu	Tyr	Val	Cys	Val	Phe	Ile	
15						20					25				

<210> 89
<211> 163
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -31...-1
<220>
<221> UNSURE
<222> 91,108,109,112,124
<223> Xaa = any one of the twenty amino acids
<400> 89

Met	Ser	Pro	Ala	Phe	Arg	Ala	Met	Asp	Val	Glu	Pro	Arg	Ala	Lys	Gly
-30						-25				-20					
Ser	Phe	Trp	Ser	Pro	Leu	Ser	Thr	Arg	Ser	Gly	Gly	Thr	His	Ala	Cys
-15					-10					-5					1
Ser	Ala	Ser	Met	Arg	Gln	Pro	Trp	Ala	Ser	Pro	Trp	Ser	Gln	Gly	Asn
			5					10					15		
Ile	Ser	Ser	Thr	Arg	Pro	Ser	Leu	Leu	Arg	Cys	Ala	Asn	Ser	Leu	Pro
			20				25					30			
Ser	Thr	Lys	Asp	Lys	Ala	Lys	Gly	Pro	Leu	Leu	Ala	Gly	His	Pro	Cys
35						40				45					
Pro	Ile	Phe	Ser	Pro	Gly	Pro	Phe	Pro	Cys	Gly	His	Arg	Glu	Val	Trp
50					55					60					65
Pro	Glu	Tyr	Pro	Thr	Pro	Ala	Pro	Leu	His	Pro	Glu	Leu	Gly	Ala	Thr
				70				75						80	
Ser	Glu	Val	Ser	Ser	Leu	Ser	Glu	His	Xaa	Phe	Pro	Cys	Ser	Ser	Arg
			85				90					95			
Gly	Leu	Ser	Arg	Leu	Ser	Asp	Ala	Gly	Ala	Xaa	Xaa	Pro	Glu	Xaa	Lys
		100					105					110			
Gly	Val	Gln	Pro	Val	Val	Cys	Lys	Ala	Leu	Xaa	Gly	Thr	Ala	Glu	Thr
	115					120					125				
Pro	Pro	Pro													
130															

<210> 90
<211> 52
<212> PRT
<213> Homo sapiens

257

<220>
 <221> SIGNAL
 <222> -32...-1
 <400> 90
 Met Leu Gly Thr Thr Gly Leu Gly Thr Gln Gly Pro Ser Gln Gln Ala
 -30 -25 -20
 Leu Gly Phe Phe Ser Phe Met Leu Leu Gly Met Gly Gly Cys Leu Pro
 -15 -10 -5
 Gly Phe Leu Leu Gln Pro Pro Asn Arg Ser Pro Thr Leu Pro Ala Ser
 1 5 10 15
 Thr Phe Ala His
 20

<210> 91
 <211> 124
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -97...-1
 <400> 91
 Met Ala Asp Asp Leu Lys Arg Phe Leu Tyr Lys Lys Leu Pro Ser Val
 -95 -90 -85
 Glu Gly Leu His Ala Ile Val Val Ser Asp Arg Asp Gly Val Pro Val
 -80 -75 -70
 Ile Lys Val Ala Asn Asp Asn Ala Pro Glu His Ala Leu Arg Pro Gly
 -65 -60 -55 -50
 Phe Leu Ser Thr Phe Ala Leu Ala Thr Asp Gln Gly Ser Lys Leu Gly
 -45 -40 -35
 Leu Ser Lys Asn Lys Ser Ile Ile Cys Tyr Tyr Asn Thr Tyr Gln Val
 -30 -25 -20
 Val Gln Phe Asn Arg Leu Pro Leu Val Val Ser Phe Ile Ala Ser Ser
 -15 -10 -5
 Ser Ala Asn Thr Gly Leu Ile Val Ser Leu Glu Lys Glu Leu Ala Pro
 1 5 10 15
 Leu Phe Glu Glu Leu Arg Gln Val Val Glu Ile Ser
 20 25

<210> 92
 <211> 230
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -24...-1
 <220>
 <221> UNSURE
 <222> 54,79
 <223> Xaa = any one of the twenty amino acids
 <400> 92
 Met Ala Ser Leu Gly Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu Leu
 -20 -15 -10
 Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp Lys Thr
 -5 1 5
 Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly Phe Ser Lys
 10 15 20
 Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly Ile Thr Gln Cys
 25 30 35 40

258

Asp	Ile	Tyr	Ser	Thr	Leu	Leu	Gly	Leu	Pro	Ala	Asp	Ile	Xaa	Ala	Ala
				45					50					55	
Gln	Ala	Met	Met	Val	Thr	Ser	Ser	Ala	Ile	Ser	Ser	Leu	Ala	Cys	Ile
		60						65					70		
Ile	Ser	Val	Val	Gly	Met	Xaa	Cys	Thr	Val	Phe	Cys	Gln	Glu	Ser	Arg
		75					80					85			
Ala	Lys	Asp	Arg	Val	Ala	Val	Ala	Gly	Gly	Val	Phe	Phe	Ile	Leu	Gly
	90					95					100				
Gly	Leu	Leu	Gly	Phe	Ile	Pro	Val	Ala	Trp	Asn	Leu	His	Gly	Ile	Leu
105					110					115					120
Arg	Asp	Phe	Tyr	Ser	Pro	Leu	Val	Pro	Asp	Ser	Met	Lys	Phe	Glu	Ile
				125					130					135	
Gly	Glu	Ala	Leu	Tyr	Leu	Gly	Ile	Ile	Ser	Ser	Leu	Phe	Ser	Leu	Ile
			140					145					150		
Ala	Gly	Ile	Ile	Leu	Cys	Phe	Ser	Cys	Ser	Ser	Gln	Arg	Asn	Arg	Ser
		155				160						165			
Asn	Tyr	Tyr	Asp	Ala	Tyr	Gln	Ala	Gln	Pro	Leu	Ala	Thr	Arg	Ser	Ser
	170					175					180				
Pro	Arg	Pro	Gly	Gln	Pro	Pro	Lys	Val	Lys	Ser	Glu	Phe	Asn	Ser	Tyr
185					190					195					200
Ser	Leu	Thr	Gly	Tyr	Val										
				205											

<210> 93
 <211> 72
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -32...-1
 <400> 93

Met	Phe	Ala	Pro	Ala	Val	Met	Arg	Ala	Phe	Arg	Lys	Asn	Lys	Thr	Leu
		-30					-25					-20			
Gly	Tyr	Gly	Val	Pro	Met	Leu	Leu	Leu	Ile	Val	Gly	Gly	Ser	Phe	Gly
	-15					-10					-5				
Leu	Arg	Glu	Phe	Ser	Gln	Ile	Arg	Tyr	Asp	Ala	Val	Lys	Ser	Lys	Met
1				5				10						15	
Asp	Pro	Glu	Leu	Glu	Lys	Lys	Pro	Lys	Glu	Asn	Lys	Ile	Ser	Leu	Glu
		20						25					30		
Ser	Glu	Tyr	Glu	Gly	Ser	Ile	Cys								
		35					40								

<210> 94
 <211> 91
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -36...-1
 <400> 94

Met	Asn	Thr	Phe	Glu	Pro	Asp	Ser	Leu	Ala	Val	Ile	Ala	Phe	Phe	Leu
	-35					-30					-25				
Pro	Ile	Trp	Thr	Phe	Ser	Ala	Leu	Thr	Phe	Leu	Phe	Leu	His	Leu	Pro
-20					-15					-10					-5
Pro	Ser	Thr	Ser	Leu	Phe	Ile	Asn	Leu	Ala	Arg	Gly	Gln	Ile	Lys	Gly
			1				5					10			
Pro	Leu	Gly	Leu	Ile	Leu	Leu	Leu	Ser	Phe	Cys	Gly	Gly	Tyr	Thr	Lys
	15					20						25			

259

Cys	Asp	Phe	Ala	Leu	Ser	Tyr	Leu	Glu	Ile	Pro	Asn	Arg	Ile	Glu	Phe
	30					35					40				
Ser	Ile	Met	Asp	Pro	Lys	Arg	Lys	Thr	Lys	Cys					
45					50					55					

<210> 95
 <211> 106
 <212> PRT
 <213> Homo sapiens
 <220>

<221> SIGNAL
 <222> -32...-1
 <400> 95

Met	Phe	Ala	Pro	Ala	Val	Met	Arg	Ala	Phe	Arg	Lys	Asn	Lys	Thr	Leu
		-30					-25					-20			
Gly	Tyr	Gly	Val	Pro	Met	Leu	Leu	Leu	Ile	Val	Gly	Gly	Ser	Phe	Gly
	-15					-10					-5				
Leu	Arg	Glu	Phe	Ser	Gln	Ile	Arg	Tyr	Asp	Ala	Val	Lys	Gly	Lys	Met
1				5					10					15	
Asp	Pro	Glu	Leu	Glu	Lys	Lys	Leu	Lys	Glu	Asn	Lys	Ile	Ser	Leu	Glu
			20					25					30		
Ser	Glu	Tyr	Glu	Lys	Ile	Lys	Asp	Ser	Lys	Phe	Asp	Asp	Trp	Lys	Asn
		35					40					45			
Ile	Arg	Gly	Pro	Arg	Pro	Trp	Glu	Asp	Pro	Asp	Leu	Leu	Gln	Gly	Arg
	50					55					60				
Asn	Pro	Glu	Ser	Leu	Lys	Thr	Lys	Thr	Thr						
65					70										

<210> 96
 <211> 172
 <212> PRT
 <213> Homo sapiens
 <220>

<221> SIGNAL
 <222> -21...-1
 <400> 96

Met	Trp	Trp	Phe	Gln	Gln	Gly	Leu	Ser	Phe	Leu	Pro	Ser	Ala	Leu	Val
	-20					-15					-10				
Ile	Trp	Thr	Ser	Ala	Ala	Phe	Ile	Phe	Ser	Tyr	Ile	Thr	Ala	Val	Thr
-5				1				5					10		
Leu	His	His	Ile	Asp	Pro	Ala	Leu	Pro	Tyr	Ile	Ser	Asp	Thr	Gly	Thr
		15					20					25			
Val	Ala	Pro	Glu	Lys	Cys	Leu	Phe	Gly	Ala	Met	Leu	Asn	Ile	Ala	Ala
	30					35					40				
Val	Leu	Cys	Ile	Ala	Thr	Ile	Tyr	Val	Arg	Tyr	Lys	Gln	Val	His	Ala
	45					50				55					
Leu	Ser	Pro	Glu	Glu	Asn	Val	Ile	Ile	Lys	Leu	Asn	Lys	Ala	Gly	Leu
60					65					70					75
Val	Leu	Gly	Ile	Leu	Ser	Cys	Leu	Gly	Leu	Ser	Ile	Val	Ala	Asn	Phe
			80					85					90		
Gln	Glu	Asn	Asn	Pro	Phe	Cys	Cys	Thr	Cys	Lys	Trp	Ser	Cys	Ala	Tyr
		95						100					105		
Leu	Trp	Tyr	Gly	Leu	Ile	Ile	Tyr	Val	Cys	Ser	Asp	His	Pro	Phe	Leu
	110					115					120				
Pro	Lys	Cys	Ser	Pro	Lys	Ser	Asn	Gly	Lys	Thr	Ser	Leu	Leu	Asp	Gln
	125					130				135					
Thr	Val	Val	Gly	Tyr	Leu	Val	Trp	Ser	Lys	Cys	Thr				
140					145					150					



1950

1951

1952

[illegible]

Met	Gln	Asn	His	Leu	Gln	Thr	Arg	Pro	Leu	Phe	Leu	Thr	Cys	Leu	Phe
		-20					-15					-10			
Trp	Pro	Leu	Ala	Ala	Leu	Asn	Val	Asn	Ser	Thr	Phe	Glu	Cys	Leu	Ile
	-5					1				5					10
Leu	Gln	Cys	Ser	Val	Phe	Ser	Phe	Ala	Phe	Phe	Ala	Leu	Trp		
				15					20						

Met	Trp	Arg	Leu	Leu	Ala	Arg	Ala	Ser	Ala	Pro	Leu	Leu	Arg	Val	Pro
			-25					-20					-15		
Leu	Ser	Asp	Ser	Trp	Ala	Leu	Leu	Pro	Ala	Ser	Ala	Gly	Val	Lys	Thr
		-10					-5					1			
Leu	Leu	Pro	Val	Pro	Ser	Phe	Glu	Asp	Val	Ser	Ile	Pro	Glu	Lys	Pro
5					10					15					20
Lys	Leu	Arg	Phe	Ile	Glu	Arg	Ala	Pro	Leu	Val	Pro	Lys	Val	Arg	Arg
			25						30					35	
Glu	Pro	Lys	Asn	Leu	Ser	Asp	Ile	Arg	Gly	Pro	Ser	Thr	Glu	Ala	Thr
			40					45					50		
Glu	Xaa	Thr	Glu	Gly	Asn	Phe	Ala	Ile	Leu	Ala	Leu	Gly	Gly	Gly	Tyr
		55					60					65			
Leu	His	Trp	Gly	His	Phe	Glu	Met	Met	Arg	Leu	Thr	Ile	Asn	Arg	Ser

261



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70		75		80
Met Asp Pro Lys Asn Met Phe Ala Ile Trp Arg Val Pro Ala Pro Phe				
85		90		100
Lys Pro Ile Thr Arg Lys Ser Val Gly His Arg Met Gly Gly Gly Lys				
	105		110	115
Gly Ala Ile Asp His Tyr Val Thr Pro Val Lys Ala Gly Arg Xaa Xaa				
	120		125	130
Val Glu Met Gly Gly Arg Cys Xaa Phe Glu Glu Val Gln Gly Phe Leu				
	135		140	145
Asp Gln Val Ala His Lys Leu Pro Phe Ala Ala Lys Ala Val Ser Arg				
	150		155	160
Gly Thr Leu Glu Lys Met Arg Lys Asp Gln Glu Glu Arg Glu Xaa Asn				
165		170		180
Asn Gln Asn Pro Trp Thr Phe Glu Arg Ile Ala Thr Ala Xaa Met Leu				
	185		190	195
Gly Ile Arg Lys Val Leu Ser Pro Tyr Asp Leu Thr His Lys Gly Lys				
	200		205	210
Xaa Trp Gly Lys Phe Tyr Met Pro Xaa Arg Val				
	215		220	

<210> 100
 <211> 77
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -30...-1
 <400> 100

Met Leu Arg Leu Asp Ile Ile Asn Ser Leu Val Thr Thr Val Phe Met		
-30	-25	-20
Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu Thr Thr Thr Leu Thr		
	-10	-5
Val Gly Gly Gly Val Phe Ala Leu Val Thr Ala Val Cys Cys Leu Ala		
	5	10
Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe Asn Pro Ser Gly Pro		
	20	25
Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu Val Leu		
35	40	45

<210> 101
 <211> 81
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31...-1
 <400> 101

Met Ser Asn Thr His Thr Val Leu Val Ser Leu Pro His Pro His Pro		
-30	-25	-20
Ala Leu Thr Cys Cys His Leu Gly Leu Pro His Pro Val Arg Ala Pro		
-15	-10	-5
Arg Pro Leu Pro Arg Val Glu Pro Trp Asp Pro Arg Trp Gln Asp Ser		
	5	10
Glu Leu Arg Tyr Pro Gln Ala Met Asn Ser Phe Leu Asn Glu Arg Ser		
	20	25
Ser Pro Cys Arg Thr Leu Arg Gln Glu Ala Ser Ala Asp Arg Cys Asp		
	35	40
Leu		45

262



25

11

11

11

11

11

11

11

50

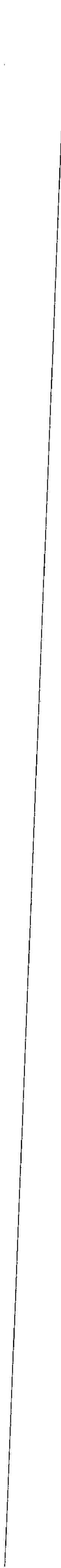
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 <211> 126
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -20...-1
 <400> 102

Met	Lys	Val	His	Met	His	Thr	Lys	Phe	Cys	Leu	Ile	Cys	Leu	Leu	Thr
-20					-15					-10					-5
Phe	Ile	Phe	His	His	Cys	Asn	His	Cys	His	Glu	Glu	His	Asp	His	Gly
			1					5					10		
Pro	Glu	Ala	Leu	His	Arg	Gln	His	Arg	Gly	Met	Thr	Glu	Leu	Glu	Pro
	15					20						25			
Ser	Lys	Phe	Ser	Lys	Gln	Ala	Ala	Glu	Asn	Glu	Lys	Lys	Tyr	Tyr	Ile
30					35					40					
Glu	Lys	Leu	Phe	Glu	Arg	Tyr	Gly	Glu	Asn	Gly	Arg	Leu	Ser	Phe	Phe
45					50					55					60
Gly	Leu	Glu	Lys	Leu	Leu	Thr	Asn	Leu	Gly	Leu	Gly	Glu	Arg	Lys	Val
				65				70						75	
Val	Glu	Ile	Asn	His	Glu	Asp	Leu	Gly	His	Asp	His	Val	Ser	His	Leu
			80					85					90		
Arg	Tyr	Phe	Gly	Ser	Ser	Arg	Gly	Lys	Ala	Phe	Ser	Leu	Thr		
		95					100					105			

<210> 103
 <211> 273
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -45...-1
 <220>
 <221> UNSURE
 <222> 181,187,193,196,198,199,203,212,214
 <223> Xaa = any one of the twenty amino acids
 <400> 103

Met	Asn	Trp	Ser	Ile	Phe	Glu	Gly	Leu	Leu	Ser	Gly	Val	Asn	Lys	Tyr
-45					-40					-35					-30
Ser	Thr	Ala	Phe	Gly	Arg	Ile	Trp	Leu	Ser	Leu	Val	Phe	Ile	Phe	Arg
				-25					-20						-15
Val	Leu	Val	Tyr	Leu	Val	Thr	Ala	Glu	Arg	Val	Trp	Ser	Asp	Asp	His
			-10					-5					1		
Lys	Asp	Phe	Asp	Cys	Asn	Thr	Arg	Gln	Pro	Gly	Cys	Ser	Asn	Val	Cys
5					10					15					
Phe	Asp	Glu	Phe	Phe	Pro	Val	Ser	His	Val	Arg	Leu	Trp	Ala	Leu	Gln
20					25					30					35
Leu	Ile	Leu	Val	Thr	Cys	Pro	Ser	Leu	Leu	Val	Val	Met	His	Val	Ala
				40				45						50	
Tyr	Arg	Glu	Val	Gln	Glu	Lys	Arg	His	Arg	Glu	Ala	His	Gly	Glu	Asn
		55				60						65			
Ser	Gly	Arg	Leu	Tyr	Leu	Asn	Pro	Gly	Lys	Lys	Arg	Gly	Gly	Leu	Trp
	70					75					80				
Trp	Thr	Tyr	Val	Cys	Ser	Leu	Val	Phe	Lys	Ala	Ser	Val	Asp	Ile	Ala
85						90					95				
Phe	Leu	Tyr	Val	Phe	His	Ser	Phe	Tyr	Pro	Lys	Tyr	Ile	Leu	Pro	Pro

263



100					105					110				115
Val	Val	Lys	Cys	His	Ala	Asp	Pro	Cys	Pro	Asn	Ile	Val	Asp	Cys
				120					125					130
Ile	Ser	Lys	Pro	Ser	Glu	Lys	Asn	Ile	Phe	Thr	Leu	Phe	Met	Val
			135					140					145	
Thr	Ala	Ala	Ile	Cys	Ile	Leu	Leu	Asn	Leu	Val	Glu	Leu	Ile	Tyr
		150					155				160			
Val	Ser	Lys	Arg	Cys	His	Glu	Cys	Leu	Ala	Ala	Arg	Lys	Ala	Gln
	165					170					175			
Met	Xaa	Thr	Gly	His	His	Pro	Xaa	Asp	Thr	Thr	Phe	Ser	Xaa	Lys
180					185					190				195
Xaa	Asp	Xaa	Xaa	Ser	Gly	Asp	Xaa	Ile	Phe	Leu	Gly	Ser	Asp	Ser
				200				205					210	
Xaa	Pro	Xaa	Leu	Pro	Asp	Arg	Pro	Arg	Asp	His	Val	Lys	Lys	Thr
			215					220					225	

Leu

<210> 104

<211> 158

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -37...-1

<400> 104

Met	Ala	Ser	Lys	Ile	Leu	Leu	Asn	Val	Gln	Glu	Glu	Val	Thr	Cys	Pro
		-35					-30					-25			
Ile	Cys	Leu	Glu	Leu	Leu	Thr	Glu	Pro	Leu	Ser	Leu	Asp	Cys	Gly	His
	-20					-15					-10				
Ser	Leu	Cys	Arg	Ala	Cys	Ile	Thr	Val	Ser	Asn	Lys	Glu	Ala	Val	Thr
-5				1				5						10	
Ser	Met	Gly	Gly	Lys	Ser	Ser	Cys	Pro	Val	Cys	Gly	Ile	Ser	Tyr	Ser
		15					20					25			
Phe	Glu	His	Leu	Gln	Ala	Asn	Gln	His	Arg	Ala	Asn	Ile	Val	Glu	Arg
	30					35					40				
Leu	Lys	Glu	Val	Lys	Leu	Ser	Pro	Asp	Asn	Gly	Lys	Lys	Arg	Asp	Leu
	45				50					55					
Cys	Asp	His	His	Gly	Glu	Lys	Leu	Leu	Leu	Phe	Cys	Lys	Glu	Asp	Arg
60				65					70					75	
Lys	Val	Ile	Cys	Trp	Leu	Cys	Glu	Arg	Ser	Gln	Glu	His	Arg	Gly	His
			80					85						90	
His	Thr	Gly	Pro	His	Gly	Gly	Ser	Ile	Gln	Gly	Met	Ser	Gly	Glu	Thr
		95					100						105		
Pro	Gly	Ser	Pro	Gln	Glu	Ala	Glu	Glu	Gly	Arg	Gly	Gly	Ser		
		110					115					120			

<210> 105

<211> 51

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -19...-1

<220>

<221> UNSURE

<222> 8

<223> Xaa = any one of the twenty amino acids

<400> 105

264

Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser Pro
 -15 -10 -5
 Val His Thr Thr Leu Ser Lys Ser Asp Ala Xaa Lys Pro Pro Gln Arg
 1 5 10
 Arg Cys Trp Arg Arg Val Ser Phe Gln Ile Ser Arg Cys Lys Thr Gly
 15 20 25
 Val Trp Trp
 30

<210> 106

<211> 359

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -34...-1

<220>

<221> UNSURE

<222> 20,64,65,130,156,282,288,289,294,296,300,302,310

<223> Xaa = any one of the twenty amino acids

<400> 106

Met Leu Leu Ser Ile Gly Met Leu Met Leu Ser Ala Thr Gln Val Tyr
 -30 -25 -20
 Thr Ile Leu Thr Val Gln Leu Phe Ala Phe Leu Asn Leu Leu Pro Val
 -15 -10 -5
 Glu Ala Asp Ile Leu Ala Tyr Asn Phe Glu Asn Ala Ser Gln Thr Phe
 1 5 10
 Asp Asp Leu Pro Ala Xaa Phe Gly Tyr Arg Leu Pro Ala Glu Gly Leu
 15 20 25 30
 Lys Gly Phe Leu Ile Asn Ser Lys Pro Glu Asn Ala Cys Glu Pro Ile
 35 40 45
 Val Pro Pro Pro Val Lys Asp Asn Ser Ser Gly Thr Phe Ile Val Leu
 50 55 60
 Ile Xaa Xaa Leu Asp Cys Asn Phe Asp Ile Lys Val Leu Asn Ala Gln
 65 70 75
 Arg Ala Gly Tyr Lys Ala Ala Ile Val His Asn Val Asp Ser Asp Asp
 80 85 90
 Leu Ile Ser Met Gly Ser Asn Asp Ile Glu Val Leu Lys Lys Ile Asp
 95 100 105 110
 Ile Pro Ser Val Phe Ile Gly Glu Ser Ser Ala Ser Ser Leu Lys Asp
 115 120 125
 Glu Phe Thr Xaa Glu Lys Gly Gly His Leu Ile Leu Val Pro Glu Phe
 130 135 140
 Ser Leu Pro Leu Glu Tyr Tyr Leu Ile Pro Phe Leu Ile Xaa Val Gly
 145 150 155
 Ile Cys Leu Ile Leu Ile Val Ile Phe Met Ile Thr Lys Leu Ser Arg
 160 165 170
 Asp Arg His Arg Ala Arg Arg Asn Arg Leu Arg Lys Asp Gln Leu Lys
 175 180 185 190
 Lys Leu Pro Val His Lys Phe Lys Lys Gly Asp Glu Tyr Asp Val Cys
 195 200 205
 Ala Ile Cys Leu Asp Glu Tyr Glu Asp Gly Asp Lys Leu Arg Ile Leu
 210 215 220
 Pro Cys Ser His Ala Tyr His Cys Lys Cys Val Asp Pro Trp Leu Thr
 225 230 235
 Lys Thr Lys Lys Thr Cys Pro Val Cys Arg Gln Lys Val Val Pro Ser
 240 245 250
 Gln Gly Asp Ser Asp Ser Asp Thr Asp Ser Ser Gln Glu Glu Asn Glu

265

255					260					265					270
Val	Thr	Glu	His	Thr	Pro	Leu	Leu	Arg	Pro	Leu	Xaa	Phe	Cys	Gln	Cys
				275					280					285	
Pro	Xaa	Xaa	Phe	Gly	Ala	Leu	Xaa	Gly	Xaa	Pro	Ala	His	Xaa	Gln	Xaa
			290					295					300		
His	Asp	Arg	Ile	Ile	Gln	Thr	Xaa	Glu	Glu	Asp	Asp	Asn	Glu	Asp	Thr
	305						310					315			
Asp	Ser	Ser	Asp	Ala	Glu	Glu									
	320					325									

<210> 107
 <211> 291
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -42..-1
 <400> 107

Met	Asp	Ser	Arg	Val	Ser	Ser	Pro	Glu	Lys	Gln	Asp	Lys	Glu	Asn	Phe
	-40						-35					-30			
Val	Gly	Val	Asn	Asn	Lys	Arg	Leu	Gly	Val	Cys	Gly	Trp	Ile	Leu	Phe
	-25					-20				-15					
Ser	Leu	Ser	Phe	Leu	Leu	Val	Ile	Ile	Thr	Phe	Pro	Ile	Ser	Ile	Trp
-10					-5				1				5		
Met	Cys	Leu	Lys	Ile	Ile	Lys	Glu	Tyr	Glu	Arg	Ala	Val	Val	Phe	Arg
		10					15					20			
Leu	Gly	Arg	Ile	Gln	Ala	Asp	Lys	Ala	Lys	Gly	Pro	Gly	Leu	Ile	Leu
	25				30					35					
Val	Leu	Pro	Cys	Ile	Asp	Val	Phe	Val	Lys	Val	Asp	Leu	Arg	Thr	Val
40					45					50					
Thr	Cys	Asn	Ile	Pro	Pro	Gln	Glu	Ile	Leu	Thr	Arg	Asp	Ser	Val	Thr
55				60					65					70	
Thr	Gln	Val	Asp	Gly	Val	Val	Tyr	Tyr	Arg	Ile	Tyr	Ser	Ala	Val	Ser
			75					80					85		
Ala	Val	Ala	Asn	Val	Asn	Asp	Val	His	Gln	Ala	Thr	Phe	Leu	Leu	Ala
		90			95							100			
Gln	Thr	Thr	Leu	Arg	Asn	Val	Leu	Gly	Thr	Gln	Thr	Leu	Ser	Gln	Ile
	105				110					115					
Leu	Ala	Gly	Arg	Glu	Glu	Ile	Ala	His	Ser	Ile	Gln	Thr	Leu	Leu	Asp
120					125					130					
Asp	Ala	Thr	Glu	Leu	Trp	Gly	Ile	Arg	Val	Ala	Arg	Val	Glu	Ile	Lys
135					140				145					150	
Asp	Val	Arg	Ile	Pro	Val	Gln	Leu	Gln	Arg	Ser	Met	Ala	Ala	Glu	Ala
			155					160						165	
Glu	Ala	Thr	Arg	Glu	Ala	Arg	Ala	Lys	Val	Leu	Ala	Ala	Glu	Gly	Glu
	170						175					180			
Met	Ser	Ala	Ser	Lys	Ser	Leu	Lys	Ser	Ala	Ser	Met	Val	Leu	Ala	Glu
	185					190						195			
Ser	Pro	Ile	Ala	Leu	Gln	Leu	Arg	Tyr	Leu	Gln	Thr	Leu	Ser	Thr	Val
	200				205				210						
Ala	Thr	Glu	Lys	Asn	Ser	Thr	Ile	Val	Phe	Pro	Leu	Pro	Met	Asn	Ile
215				220					225					230	
Leu	Glu	Gly	Ile	Gly	Gly	Val	Ser	Tyr	Asp	Asn	His	Lys	Lys	Leu	Pro
			235					240						245	
Asn	Lys	Ala													

<210> 108
 <211> 67

266

Ala	Leu	Val	Asp	Glu	Leu	Glu	Trp	Glu	Ile	Ala	Gln	Val	Asp	Pro	Lys
	15					20					25				
Lys	Thr	Ile	Gln	Met	Gly	Ser	Phe	Arg	Ile	Asn	Pro	Asp	Gly	Ser	Gln
	30				35					40					
Ser	Val	Val	Glu	Val	Thr	Val	Thr	Xaa	Ser	Pro	Lys	Thr	Lys	Val	Ala
45				50					55						60
His	Ser	Gly	Phe	Trp	Met	Lys	Ile	Arg	Leu	Leu	Lys	Lys	Gly	Pro	Trp
				65				70						75	

Ser

<210> 111
 <211> 86
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -20...-1
 <400> 111

Met	Lys	Gly	Trp	Gly	Trp	Leu	Ala	Leu	Leu	Leu	Gly	Ala	Leu	Leu	Gly
-20				-15				-10							-5
Thr	Ala	Trp	Ala	Arg	Arg	Ser	Gln	Asp	Leu	His	Cys	Gly	Ala	Cys	Arg
			1				5					10			
Ala	Leu	Val	Asp	Glu	Thr	Arg	Met	Gly	Asn	Cys	Pro	Gly	Gly	Pro	Gln
	15					20					25				
Glu	Asp	His	Ser	Asp	Gly	Ile	Phe	Pro	Asp	Gln	Ser	Arg	Trp	Gln	Pro
30					35					40					
Val	Ser	Gly	Gly	Gly	Ala	Leu	Cys	Pro	Leu	Arg	Gly	Pro	Pro	His	Arg
45				50				55							60
Ala	Ala	Gly	Gly	Asp	Met										
				65											

<210> 112
 <211> 71
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -25...-1
 <400> 112

Met	Pro	Ala	Gly	Val	Pro	Met	Ser	Thr	Tyr	Leu	Lys	Met	Phe	Ala	Ala
-25				-20				-15							-10
Ser	Leu	Leu	Ala	Met	Cys	Ala	Gly	Ala	Glu	Val	Val	His	Arg	Tyr	Tyr
			-5					1				5			
Arg	Pro	Asp	Leu	Thr	Ile	Pro	Glu	Ile	Pro	Pro	Lys	Arg	Gly	Glu	Leu
	10					15					20				
Lys	Thr	Glu	Leu	Leu	Gly	Leu	Lys	Glu	Arg	Lys	His	Lys	Pro	Gln	Val
25					30					35					
Ser	Gln	Gln	Glu	Glu	Leu	Lys									
40					45										

<210> 113
 <211> 60
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -42...-1
 <400> 113



Met	Asp	Gly	His	Trp	Ser	Ala	Ala	Phe	Ser	Ala	Leu	Thr	Val	Thr	Ala
		-40					-35					-30			
Met	Ser	Ser	Trp	Ala	Arg	Arg	Arg	Ser	Ser	Ser	Ser	Arg	Arg	Ile	Pro
	-25					-20				-15					
Ser	Leu	Pro	Gly	Ser	Pro	Val	Cys	Trp	Ala	Trp	Pro	Trp	Tyr	Pro	Asp
-10					-5					1				5	
Thr	Thr	Ser	Phe	Pro	Leu	Arg	Cys	Arg	Gly	Arg	Val				
			10					15							

<210> 114
 <211> 118
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -83...-1
 <220>

<221> UNSURE
 <222> 28,32

<223> Xaa = any one of the twenty amino acids

<400> 114

Met	Leu	Pro	Val	Gln	Ser	Phe	Thr	Leu	Val	Ala	Gln	Ala	Gly	Val	Gln
			-80					-75					-70		
Trp	Arg	His	Leu	Ser	Ser	Leu	Gln	Leu	Leu	Pro	Pro	Glu	Phe	Lys	Gly
		-65					-60					-55			
Phe	Ser	Cys	Leu	Ser	Leu	Pro	Ser	Ser	Trp	Asp	Tyr	Arg	Arg	Pro	Pro
	-50					-45				-40					
Pro	Cys	Pro	Ala	Gly	Phe	Phe	Val	Phe	Leu	Val	Glu	Thr	Gly	Leu	His
-35					-30					-25					-20
His	Val	Gly	Gln	Ala	Gly	Leu	Glu	Leu	Leu	Thr	Ser	Cys	Ser	Pro	Pro
			-15					-10						-5	
Ala	Ser	Ala	Ser	Gln	Ser	Ala	Ala	Ile	Thr	Gly	Val	Ser	His	Val	Pro
			1				5					10			
Gly	Lys	Lys	Lys	Leu	Leu	Lys	Val	Glu	Lys	Lys	Asn	Leu	Arg	Xaa	Leu
15						20					25				
Leu	Thr	Xaa	Ile	Lys	Thr										
30					35										

<210> 115
 <211> 76
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22...-1
 <220>

<221> UNSURE
 <222> 22,43

<223> Xaa = any one of the twenty amino acids

<400> 115

Met	Glu	Leu	Ile	Ser	Pro	Thr	Val	Ile	Ile	Ile	Leu	Gly	Cys	Leu	Ala
		-20					-15					-10			
Leu	Phe	Leu	Leu	Leu	Gln	Arg	Lys	Asn	Leu	Arg	Arg	Pro	Pro	Cys	Ile
	-5					1				5				10	
Lys	Gly	Trp	Ile	Pro	Trp	Ile	Gly	Val	Gly	Phe	Xaa	Phe	Gly	Lys	Ala
			15				20						25		
Pro	Leu	Glu	Phe	Ile	Glu	Lys	Ala	Arg	Ile	Lys	Val	Cys	Gly	Arg	Gly
			30					35					40		

269

Xaa Arg Gly Leu Gln Arg Arg Gln Cys Phe Leu Phe
 45 50

<210> 116
 <211> 95
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -52...-1
 <400> 116

Met	Ala	Glu	Thr	Lys	Asp	Ala	Ala	Gln	Met	Leu	Val	Thr	Phe	Lys	Asp
	-50					-45					-40				
Val	Ala	Val	Thr	Phe	Thr	Arg	Glu	Glu	Trp	Arg	Gln	Leu	Asp	Leu	Ala
	-35					-30					-25				
Gln	Arg	Thr	Leu	Tyr	Arg	Glu	Val	Met	Leu	Glu	Thr	Cys	Gly	Leu	Leu
	-20				-15					-10					-5
Val	Ser	Leu	Gly	Gln	Ser	Ile	Trp	Leu	His	Ile	Thr	Glu	Asn	Gln	Ile
			1				5						10		
Lys	Leu	Ala	Ser	Pro	Gly	Arg	Lys	Phe	Thr	Asn	Ser	Pro	Asp	Glu	Lys
	15					20					25				
Pro	Glu	Val	Trp	Leu	Ala	Pro	Gly	Leu	Phe	Gly	Ala	Ala	Ala	Gln	
	30					35					40				

<210> 117
 <211> 82
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -22...-1
 <400> 117

Met	Glu	Leu	Ile	Ser	Pro	Thr	Val	Ile	Ile	Ile	Leu	Gly	Cys	Leu	Ala
	-20					-15					-10				
Leu	Phe	Leu	Leu	Leu	Gln	Arg	Lys	Asn	Leu	Arg	Arg	Pro	Pro	Cys	Ile
	-5				1				5						10
Lys	Gly	Trp	Ile	Pro	Trp	Ile	Gly	Val	Gly	Phe	Glu	Phe	Gly	Lys	Ala
			15					20					25		
Pro	Leu	Glu	Phe	Ile	Glu	Lys	Ala	Arg	Ile	Lys	Tyr	Gly	Pro	Ile	Phe
		30					35					40			
Thr	Val	Phe	Ala	Met	Gly	Asn	Arg	Met	Thr	Phe	Val	Thr	Glu	Glu	Gly
	45					50						55			
Arg	Asn														
	60														

<210> 118
 <211> 89
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -16...-1
 <400> 118

Met	Ile	Ile	Ser	Leu	Phe	Ile	Tyr	Ile	Phe	Leu	Thr	Cys	Ser	Asn	Thr
	-15					-10					-5				
Ser	Pro	Ser	Tyr	Gln	Gly	Thr	Gln	Leu	Gly	Leu	Gly	Leu	Pro	Ser	Ala
1			5					10					15		
Gln	Trp	Trp	Pro	Leu	Thr	Gly	Arg	Arg	Met	Gln	Cys	Cys	Arg	Leu	Phe

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		20					25				30				
Cys	Phe	Leu	Leu	Gln	Asn	Cys	Leu	Phe	Pro	Phe	Pro	Leu	His	Leu	Ile
		35					40					45			
Gln	His	Asp	Pro	Cys	Glu	Leu	Val	Leu	Thr	Ile	Ser	Trp	Asp	Trp	Ala
	50					55					60				
Glu	Ala	Gly	Ala	Ser	Leu	Tyr	Ser	Pro							
65					70										

<210> 119
 <211> 30
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -19...-1
 <400> 119

Met	Thr	Met	Ala	Glu	Cys	Pro	Thr	Leu	Cys	Val	Ser	Ser	Ser	Pro	Ala
				-15					-10					-5	
Leu	Trp	Ala	Ala	Ser	Glu	Thr	Thr	Asp	Asp	Val	Cys	Arg	Glu		
		1				5						10			

<210> 120
 <211> 115
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -103...-1
 <400> 120

Met	Val	Ile	Arg	Val	Tyr	Ile	Ala	Ser	Ser	Ser	Gly	Ser	Thr	Ala	Ile
			-100					-95					-90		
Lys	Lys	Lys	Gln	Gln	Asp	Val	Leu	Gly	Phe	Leu	Glu	Ala	Asn	Lys	Ile
		-85					-80					-75			
Gly	Phe	Glu	Glu	Lys	Asp	Ile	Ala	Ala	Asn	Glu	Glu	Asn	Arg	Lys	Trp
	-70					-65					-60				
Met	Arg	Glu	Asn	Val	Pro	Glu	Asn	Ser	Arg	Pro	Ala	Thr	Gly	Asn	Pro
-55					-50				-45					-40	
Leu	Pro	Pro	Gln	Ile	Phe	Asn	Glu	Ser	Gln	Tyr	Arg	Gly	Asp	Tyr	Asp
			-35					-30					-25		
Ala	Phe	Phe	Glu	Ala	Arg	Glu	Asn	Asn	Ala	Val	Tyr	Ala	Phe	Leu	Gly
		-20					-15					-10			
Leu	Thr	Ala	Pro	Ser	Gly	Ser	Lys	Glu	Ala	Gly	Arg	Cys	Lys	Gln	Ser
	-5					1				5					
Ser	Lys	Pro													
10															

<210> 121
 <211> 105
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -76...-1
 <400> 121

Met	Pro	Leu	Leu	Cys	Gln	Ile	Glu	Met	Glu	Tyr	Leu	Leu	Leu	Lys	Trp
	-75					-70				-65					
Gln	Met	Thr	Met	Leu	Gln	Ser	Met	Leu	Cys	Asp	Leu	Val	Ser	Tyr	Pro
-60					-55					-50					-45

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Leu	Leu	Pro	Leu	Gln	Gln	Thr	Lys	Glu	Ala	Asn	Leu	Asp	Phe	Pro	Lys
				-40					-35					-30	
Ile	Lys	Val	Ser	Ser	Val	Thr	Ile	Thr	Pro	Thr	Arg	Trp	Phe	Asn	Leu
			-25					-20					-15		
Ile	Val	Tyr	Leu	Trp	Val	Val	Ser	Phe	Ile	Ala	Ser	Ser	Ser	Ala	Asn
		-10					-5					1			
Thr	Gly	Leu	Ile	Val	Ser	Leu	Glu	Lys	Glu	Leu	Ala	Pro	Leu	Phe	Glu
5					10					15					20
Glu	Leu	Arg	Gln	Val	Val	Glu	Val	Ser							
				25											

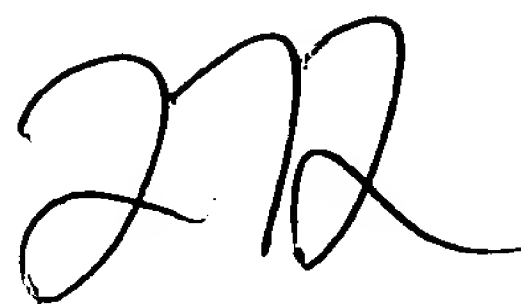
<210> 122
 <211> 93
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -22...-1
 <400> 122

Met	Lys	Pro	Val	Leu	Pro	Leu	Gln	Phe	Leu	Val	Val	Phe	Cys	Leu	Ala
		-20					-15					-10			
Leu	Gln	Leu	Val	Pro	Gly	Ser	Pro	Lys	Gln	Arg	Val	Leu	Lys	Tyr	Ile
	-5					1				5					10
Leu	Glu	Pro	Pro	Pro	Cys	Ile	Ser	Ala	Pro	Glu	Asn	Cys	Thr	His	Leu
				15					20					25	
Cys	Thr	Met	Gln	Glu	Asp	Cys	Glu	Lys	Gly	Phe	Gln	Cys	Cys	Ser	Ser
			30					35					40		
Phe	Cys	Gly	Ile	Val	Cys	Ser	Ser	Glu	Thr	Phe	Gln	Lys	Arg	Asn	Arg
		45					50					55			
Ile	Lys	His	Lys	Gly	Ser	Glu	Val	Ile	Met	Pro	Ala	Asn			
	60					65					70				

<210> 123
 <211> 109
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -42...-1
 <400> 123

Met	His	Ile	Leu	Gln	Leu	Leu	Thr	Thr	Val	Asp	Asp	Gly	Ile	Gln	Ala
		-40					-35					-30			
Ile	Val	His	Cys	Pro	Asp	Thr	Gly	Lys	Asp	Ile	Trp	Asn	Leu	Leu	Phe
	-25					-20					-15				
Asp	Leu	Val	Cys	His	Glu	Phe	Cys	Gln	Ser	Asp	Asp	Pro	Ala	Ile	Ile
-10					-5					1				5	
Leu	Gln	Glu	Gln	Lys	Thr	Val	Leu	Ala	Ser	Val	Phe	Ser	Val	Leu	Ser
			10					15					20		
Ala	Ile	Tyr	Ala	Ser	Gln	Thr	Glu	Gln	Glu	Tyr	Leu	Lys	Ile	Glu	Lys
	25					30						35			
Val	Asp	Leu	Pro	Leu	Ile	Asp	Ser	Leu	Ile	Arg	Val	Leu	Gln	Asn	Met
	40					45					50				
Glu	Gln	Cys	Gln	Lys	Lys	Pro	Glu	Asn	Ser	Ala	Gly	Val			
55					60					65					

<210> 124
 <211> 51
 <212> PRT



<213> Homo sapiens

<220>

<221> SIGNAL

<222> -15...-1

<400> 124

Met	Arg	Leu	Val	Pro	Leu	Gly	Gln	Ser	Phe	Pro	Leu	Ser	Glu	Pro	Arg
-15					-10				-5						1
Cys	Leu	Gln	Pro	Val	Lys	Trp	Asp	His	Asn	His	Cys	Leu	Thr	Ser	Leu
		5					10						15		
Thr	Val	Val	Val	Arg	Thr	Glu	Cys	Val	Glu	Val	Phe	His	Lys	Leu	Trp
		20				25						30			
Met	Leu	Val													
		35													

<210> 125

<211> 56

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -27...-1

<400> 125

Met	Asn	Arg	Val	Pro	Ala	Asp	Ser	Pro	Asn	Met	Cys	Leu	Ile	Cys	Leu
	-25					-20					-15				
Leu	Ser	Tyr	Ile	Ala	Leu	Gly	Ala	Ile	His	Ala	Lys	Ile	Cys	Arg	Arg
-10					-5					1				5	
Ala	Phe	Gln	Glu	Glu	Gly	Arg	Ala	Asn	Ala	Lys	Thr	Gly	Val	Arg	Ala
			10				15							20	
Trp	Cys	Ile	Gln	Pro	Trp	Ala	Lys								
			25												

<210> 126

<211> 162

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -21...-1

<400> 126

Met	Leu	Gln	Thr	Ser	Asn	Tyr	Ser	Leu	Val	Leu	Ser	Leu	Gln	Phe	Leu
-20					-15					-10					
Leu	Leu	Ser	Tyr	Asp	Leu	Phe	Val	Asn	Ser	Phe	Ser	Glu	Leu	Leu	Gln
-5				1				5					10		
Lys	Thr	Pro	Val	Ile	Gln	Leu	Val	Leu	Phe	Ile	Ile	Gln	Asp	Ile	Ala
		15					20					25			
Val	Leu	Phe	Asn	Ile	Ile	Ile	Ile	Phe	Leu	Met	Phe	Phe	Asn	Thr	Ser
	30					35					40				
Val	Phe	Gln	Ala	Gly	Leu	Val	Asn	Leu	Leu	Phe	His	Lys	Phe	Lys	Gly
45					50					55					
Thr	Ile	Ile	Leu	Thr	Ala	Val	Tyr	Phe	Ala	Leu	Ser	Ile	Ser	Leu	His
60				65				70						75	
Val	Trp	Val	Met	Asn	Leu	Arg	Trp	Lys	Asn	Ser	Asn	Ser	Phe	Ile	Trp
			80					85					90		
Thr	Asp	Gly	Leu	Gln	Met	Leu	Phe	Val	Phe	Gln	Arg	Leu	Ala	Ala	Val
		95					100						105		
Leu	Tyr	Cys	Tyr	Phe	Tyr	Lys	Arg	Thr	Ala	Val	Arg	Leu	Gly	Asp	Pro
		110				115						120			
His	Phe	Tyr	Gln	Asp	Ser	Leu	Trp	Leu	Arg	Lys	Glu	Phe	Met	Gln	Val

125
Arg Arg
140

130

135

<210> 127
<211> 126
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -68...-1
<400> 127

Met	Ala	Ser	Ala	Ser	Ala	Arg	Gly	Asn	Gln	Asp	Lys	Asp	Ala	His	Phe
			-65					-60					-55		
Pro	Pro	Pro	Ser	Lys	Gln	Ser	Leu	Leu	Phe	Cys	Pro	Lys	Ser	Lys	Leu
		-50					-45					-40			
His	Ile	His	Arg	Ala	Glu	Ile	Ser	Lys	Ile	Met	Arg	Glu	Cys	Gln	Glu
	-35					-30				-25					
Glu	Ser	Phe	Trp	Lys	Arg	Ala	Leu	Pro	Phe	Ser	Leu	Val	Ser	Met	Leu
-20					-15					-10					-5
Val	Thr	Gln	Gly	Leu	Val	Tyr	Gln	Gly	Tyr	Leu	Ala	Ala	Asn	Ser	Arg
			1				5					10			
Phe	Gly	Ser	Leu	Pro	Lys	Val	Ala	Leu	Ala	Gly	Leu	Leu	Gly	Phe	Gly
	15					20					25				
Leu	Gly	Lys	Val	Ser	Tyr	Ile	Gly	Val	Cys	Gln	Ser	Lys	Phe	His	Phe
30						35				40					
Phe	Glu	Asp	Gln	Leu	Arg	Gly	Ala	Gly	Phe	Gly	Pro	Thr	Ala		
45					50					55					

<210> 128
<211> 140
<212> PRT
<213> Homo sapiens
<220>
<221> SIGNAL
<222> -40...-1
<400> 128

Met	Thr	Ser	Met	Thr	Gln	Ser	Leu	Arg	Glu	Val	Ile	Lys	Ala	Met	Thr
-40					-35					-30					-25
Lys	Ala	Arg	Asn	Phe	Glu	Arg	Val	Leu	Gly	Lys	Ile	Thr	Leu	Val	Ser
			-20						-15					-10	
Ala	Ala	Pro	Gly	Lys	Val	Ile	Cys	Glu	Met	Lys	Val	Glu	Glu	Glu	His
		-5					1				5				
Thr	Asn	Ala	Ile	Gly	Thr	Leu	His	Gly	Gly	Leu	Thr	Ala	Thr	Leu	Val
10					15					20					
Asp	Asn	Ile	Ser	Thr	Met	Ala	Leu	Leu	Cys	Thr	Glu	Arg	Gly	Ala	Pro
25					30					35					40
Gly	Val	Ser	Val	Asp	Met	Asn	Ile	Thr	Tyr	Met	Ser	Pro	Ala	Lys	Leu
			45						50					55	
Gly	Glu	Asp	Ile	Val	Ile	Thr	Ala	His	Val	Leu	Lys	Gln	Gly	Lys	Thr
		60					65					70			
Leu	Ala	Phe	Thr	Ser	Val	Gly	Leu	Thr	Asn	Lys	Ala	Thr	Gly	Lys	Leu
		75					80					85			
Ile	Ala	Gln	Gly	Arg	His	Thr	Lys	His	Leu	Gly	Asn				
90						95					100				

<210> 129
<211> 43

274

<400> 132
 Met Arg Leu Pro Pro Ala Leu Pro Ser Gly Tyr Thr Asp Ser Thr Ala
 -45 -40 -35
 Leu Glu Gly Leu Val Tyr Tyr Leu Asn Gln Lys Leu Leu Phe Ser Ser
 -30 -25 -20
 Pro Ala Ser Ala Leu Leu Phe Phe Ala Arg Pro Cys Val Phe Cys Phe
 -15 -10 -5 1
 Lys Ala Ser Lys Met Gly Pro Gln Phe Glu Asn Tyr Pro Thr Phe Pro
 5 10 15
 Thr Tyr Ser Pro Leu Pro Ile Ile Pro Phe Gln Leu His Gly Arg Phe
 20 25 30

<210> 133
 <211> 53
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -42...-1

<400> 133
 Met Asp Ser Arg Val Ser Ser Pro Glu Lys Gln Asp Lys Glu Asn Phe
 -40 -35 -30
 Val Gly Val Asn Asn Lys Arg Leu Gly Val Cys Gly Trp Ile Leu Phe
 -25 -20 -15
 Ser Leu Ser Phe Leu Leu Val Ile Ile Thr Phe Pro Ile Ser Ile Trp
 -10 -5 1 5
 Met Cys Leu Lys Ile
 10

<210> 134
 <211> 1053
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> sig_peptide
 <222> 131..169
 <223> Von Heijne matrix
 score 4.19999980926514
 seq MLAVSLTVPLLGA/MM
 <220>
 <221> polyA_site
 <222> 1042..1053

<400> 134
 gagcgagtcg gacgggctgc gacagcgccg gccctgcgg ccgcaggctcg tcacagacga 60
 tgatggccag gcccggagg ctaaggacgg cagctccttt agcggcagag ttttccgagt 120
 gaccttcttg atg ctg gct gtt tct ctc acc gtt ccc ctg ctt gga gcc 169
 Met Leu Ala Val Ser Leu Thr Val Pro Leu Leu Gly Ala
 -10 -5
 atg atg ctg ctg gaa tct cct ata gat cca cag cct ctc agc ttc aaa 217
 Met Met Leu Leu Glu Ser Pro Ile Asp Pro Gln Pro Leu Ser Phe Lys
 1 5 10 15
 gaa ccc ccg ctc ttg ctt ggt gtt ctg cat cca aat acg aag ctg cga 265
 Glu Pro Pro Leu Leu Leu Gly Val Leu His Pro Asn Thr Lys Leu Arg
 20 25 30
 cag gca gaa agg ctg ttt gaa aat caa ctt gtt gga ccg gag tcc ata 313
 Gln Ala Glu Arg Leu Phe Glu Asn Gln Leu Val Gly Pro Glu Ser Ile
 35 40 45
 gca cat att ggg gat gtg atg ttt act ggg aca gca gat ggc cgg gtc 361



2

3

Ala	His	Ile	Gly	Asp	Val	Met	Phe	Thr	Gly	Thr	Ala	Asp	Gly	Arg	Val		
50						55					60						
gta	aaa	ctt	gaa	aat	ggt	gaa	ata	gag	acc	att	gcc	cgg	ttt	ggt	tcg	409	
Val	Lys	Leu	Glu	Asn	Gly	Glu	Ile	Glu	Thr	Ile	Ala	Arg	Phe	Gly	Ser		
65					70					75					80		
ggc	cct	tgc	aaa	acc	cga	ggt	gat	gag	cct	gtg	tgt	ggg	aga	ccc	ctg	457	
Gly	Pro	Cys	Lys	Thr	Arg	Gly	Asp	Glu	Pro	Val	Cys	Gly	Arg	Pro	Leu		
				85					90					95			
ggt	atc	cgt	gca	ggg	ccc	aat	ggg	act	ctc	ttt	gtg	gcc	gat	gca	tac	505	
Gly	Ile	Arg	Ala	Gly	Pro	Asn	Gly	Thr	Leu	Phe	Val	Ala	Asp	Ala	Tyr		
			100					105					110				
aag	gga	cta	ttt	gaa	gta	aat	ccc	tgg	aaa	cgt	gaa	gtg	aaa	ctg	ctg	553	
Lys	Gly	Leu	Phe	Glu	Val	Asn	Pro	Trp	Lys	Arg	Glu	Val	Lys	Leu	Leu		
		115					120					125					
ctg	tcc	tcc	gag	aca	ccc	att	gag	ggg	aag	aac	atg	tcc	ttt	gtg	aat	601	
Leu	Ser	Ser	Glu	Thr	Pro	Ile	Glu	Gly	Lys	Asn	Met	Ser	Phe	Val	Asn		
		130				135					140						
gat	ctt	aca	gtc	act	cag	gat	ggg	agg	aag	att	tat	ttc	acc	gat	tct	649	
Asp	Leu	Thr	Val	Thr	Gln	Asp	Gly	Arg	Lys	Ile	Tyr	Phe	Thr	Asp	Ser		
145					150					155					160		
agc	agc	aaa	tgg	caa	aga	cga	gac	tac	ctg	ctt	ctg	gtg	atg	gag	ggc	697	
Ser	Ser	Lys	Trp	Gln	Arg	Arg	Asp	Tyr	Leu	Leu	Leu	Val	Met	Glu	Gly		
				165					170					175			
aca	gat	gac	ggg	cgc	ctg	ctg	gag	tat	gat	act	gtg	acc	agg	gaa	gta	745	
Thr	Asp	Asp	Gly	Arg	Leu	Leu	Glu	Tyr	Asp	Thr	Val	Thr	Arg	Glu	Val		
			180					185					190				
aaa	gtt	tta	ttg	gac	cag	ctg	cgg	ttc	ccg	aat	gga	gtc	cag	ctg	tct	793	
Lys	Val	Leu	Leu	Asp	Gln	Leu	Arg	Phe	Pro	Asn	Gly	Val	Gln	Leu	Ser		
		195					200					205					
cct	gca	gaa	gac	ttt	gtc	ctg	gtg	gca	gaa	aca	acc	atg	gcc	agg	ata	841	
Pro	Ala	Glu	Asp	Phe	Val	Leu	Val	Ala	Glu	Thr	Thr	Met	Ala	Arg	Ile		
		210				215					220						
cga	aga	gtc	tac	gtt	tct	ggc	ctg	atg	aag	ggc	ggg	gct	gat	ctg	ttt	889	
Arg	Arg	Val	Tyr	Val	Ser	Gly	Leu	Met	Lys	Gly	Gly	Ala	Asp	Leu	Phe		
225					230					235					240		
gtg	gag	aac	atg	cct	gga	ttt	cca	gac	aac	atc	cgg	ccc	agc	agc	tct	937	
Val	Glu	Asn	Met	Pro	Gly	Phe	Pro	Asp	Asn	Ile	Arg	Pro	Ser	Ser	Ser		
				245					250					255			
ggg	ggg	tac	tgg	gtg	ggc	atg	tcg	acc	atc	cgc	cct	aac	cct	ggg	ttt	985	
Gly	Gly	Tyr	Trp	Val	Gly	Met	Ser	Thr	Ile	Arg	Pro	Asn	Pro	Gly	Phe		
			260				265						270				
tcc	atg	ctg	gat	ttc	tta	tct	gag	aga	ccc	tgg	att	aaa	agg	atg	att	1033	
Ser	Met	Leu	Asp	Phe	Leu	Ser	Glu	Arg	Pro	Trp	Ile	Lys	Arg	Met	Ile		
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Phe	Lys	Val															
		290															

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Met Met Tyr Val Ser
1 5
ata gaa atg tca ggt cca acc att tcc cat ttg ttc gac tat gtg gtc 162
Ile Glu Met Ser Gly Pro Thr Ile Ser His Leu Phe Asp Tyr Val Val
10 15 20
tgt tac att tat ggc tta aag tcc ttt tct ctt aaa cag tta aaa aaa 210
Cys Tyr Ile Tyr Gly Leu Lys Ser Phe Ser Leu Lys Gln Leu Lys Lys
25 30 35
aaa tct tgg tct aag tat tta ttt gaa tcc tgt tgc tat agg agt ttg 258
Lys Ser Trp Ser Lys Tyr Leu Phe Glu Ser Cys Cys Tyr Arg Ser Leu
40 45 50
tat gtg tgt gtc ttc att taaacatacc tgcatacaaa gatgggtttat 306
Tyr Val Cys Val Phe Ile
55
ttctatttaa tatgtgacat ttgtttcctg gatatagtcc gtgaaccaca agattttatca 366
tatttttcaa taatatgaga agaaaatggg ccgtaaattg ttaaccattt tatgttcaga 426
tattttctcta gttttttacct agtttgcttt aacatagaga ccagcaagtg aatatatatg 486
cataacctta tatgttgaca caataattca gaataatttg ttaaagataa actaattttt 546
cagagaagaa catttaaagg gttaaatattt ttgaaacgtt ttcagataat atctatttga 606
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aaaaaaaa 675

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seq GVLLEPFVHQVGG/HS
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<221> polyA_signal
<222> 1080..1085
<220>
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<222> 1101..1112
<400> 136

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ccgctggact ccgctgcctc ccccatctcc ccgccatctg cgcccggagg atg agc 116
Met Ser
cca gcc ttc agg gcc atg gat gtg gag ccc cgc gcc aaa ggc gtc ctt 164
Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly Val Leu
-25 -20 -15
ctg gag ccc ttt gtc cac cag gtc ggg ggg cac tca tgc gtg ctc cgc 212
Leu Glu Pro Phe Val His Gln Val Gly Gly His Ser Cys Val Leu Arg
-10 -5 1 5
ttc aat gag aca acc ctg tgc aag ccc ctg gtc cca agg gaa cat cag 260
Phe Asn Glu Thr Thr Leu Cys Lys Pro Leu Val Pro Arg Glu His Gln
10 15 20
ttc tac gag acc ctc cct gct gag atg cgc aaa ttc tct ccc cag tac 308
Phe Tyr Glu Thr Leu Pro Ala Glu Met Arg Lys Phe Ser Pro Gln Tyr
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aaa gga caa agc caa agg ccc ctt gtt agc tgg cca tcc ctg ccc cat 356

278

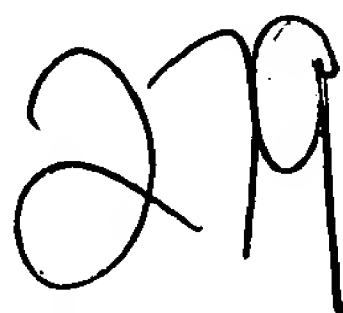
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Phe	Phe	Pro	Trp	Ser	Phe	Pro	Leu	Trp	Pro	Gln	Gly	Ser	Val	Ala		
55					60					65						
tgaatacccc	accccggtc	ctctgcaccc	agagctggg	gccacctcag	aagtgtcatc											461
tctctctgag	cacgcattcc	cctgcagcag	tcgaggactg	agcagattga	gtgatgctgg											521
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aaccagctct	atctgccttg	tgttcatttt	gttattttgt	gacgtgagac	agcaaagacc											761
aataaaaaaca	tattttataa	gaacaaaagg	cctgggtgcc	taccctgtgtg	ggggcactgt											821
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gctttgctta	cccagctctc	ccttactctt	ggatgcttct	taaccctcag	gcaaacctgt											941
gttccccctg	tattcaggct	ctgctttaaa	gcaagccatg	aggctgttgg	agtttctgtt											1001
tagggcatta	aaaattcccc	caaactataa	agagcaatgt	tttcagtcct	ttaggattag											1061
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ggttttattg	tgagctggcc	ttggaattaa	accaccacca	acacactttt	ggattatcag		180
aaggtggaag	gagtgcaaaa	atgtcattcc	catgcttgtc	tgccaggcaa	cctgggtgtcc		240
attctttatg	acgcctttcc	tgaatcacag	gtgcattggg	gtgcttcctc	ctccccagga		300
ctcccaccca	actttgtgaa	cacaacccac	ttagaggagt	tatctcagca	cattatga		358
atg ttg ggg acc acg ggc ctc ggg aca cag ggt cct tcc cag cag gct							406
Met Leu Gly Thr Thr Gly Leu Gly Thr Gln Gly Pro Ser Gln Gln Ala							
-30		-25		-20			
ctg ggc ttt ttc tcc ttt atg tta ctt gga atg ggc ggg tgc ctg cct							454
Leu Gly Phe Phe Ser Phe Met Leu Leu Gly Met Gly Gly Cys Leu Pro							
-15		-10		-5			
gga ttc ctg cta cag cct ccc aat cga tct cct act ttg cct gca tcc							502
Gly Phe Leu Leu Gln Pro Pro Asn Arg Ser Pro Thr Leu Pro Ala Ser							
1	5	10	15				
acc ttt gcc cat taaagtcaat tctccaccca taaaaaaaaa aaa							547
Thr Phe Ala His							
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<223> Von Heijne matrix
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<222> 1164..1169

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<221> polyA_site

<222> 1187..1198

<400> 138

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					-95					-90						
tat	aaa	aag	tta	cca	agt	ggt	gaa	ggg	ctc	cat	gcc	att	ggt	gtg	tca	100
Tyr	Lys	Lys	Leu	Pro	Ser	Val	Glu	Gly	Leu	His	Ala	Ile	Val	Val	Ser	
			-85				-80				-75					
gat	aga	gat	gga	gta	cct	ggt	ggt	aaa	gtg	gca	aat	gac	aat	gct	cca	148
Asp	Arg	Asp	Gly	Val	Pro	Val	Val	Lys	Val	Ala	Asn	Asp	Asn	Ala	Pro	
		-70				-65				-60						
gag	cat	gct	ttg	cga	cct	ggt	ttc	tta	tcc	act	ttt	gcc	ctt	gca	aca	196
Glu	His	Ala	Leu	Arg	Pro	Gly	Phe	Leu	Ser	Thr	Phe	Ala	Leu	Ala	Thr	
	-55				-50		-45									
gac	caa	gga	agc	aaa	ctt	gga	ctt	tcc	aaa	aat	aaa	agt	atc	atc	tgt	244
Asp	Gln	Gly	Ser	Lys	Leu	Gly	Leu	Ser	Lys	Asn	Lys	Ser	Ile	Ile	Cys	
-40			-35				-30			-25						
tac	tat	aac	acc	tac	cag	gtg	ggt	caa	ttt	aat	cgt	tta	cct	ttg	gtg	292
Tyr	Tyr	Asn	Thr	Tyr	Gln	Val	Val	Gln	Phe	Asn	Arg	Leu	Pro	Leu	Val	
		-20			-15		-10									
gtg	agt	ttc	ata	gcc	agc	agc	agt	gcc	aat	aca	gga	cta	att	gtc	agc	340
Val	Ser	Phe	Ile	Ala	Ser	Ser	Ser	Ala	Asn	Thr	Gly	Leu	Ile	Val	Ser	
	-5				1		5									
cta	gaa	aag	gag	ctt	gct	cca	ttg	ttt	gaa	gaa	ctg	aga	caa	ggt	gtg	388
Leu	Glu	Lys	Glu	Leu	Ala	Pro	Leu	Phe	Glu	Glu	Leu	Arg	Gln	Val	Val	
	10				15		20									
gaa	ggt	tct	taatctgaca	gtgggtttcag	tgtgtacctt	atctttcatta										437
Glu	Val	Ser														
25																
taacaacaca	atatcaatcc	agcaatcttt	agactacaat	aatgcttttta	tccatgtgct											497
caagaaaggg	cccctttttc	caacttatac	taaagagcta	gcatatagat	gtaattttata											557
gatagatcag	ttgctatatt	ttctgggtgta	gggtctttct	tatttagtga	gatctaggga											617
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ggatgagaga	ttctatttcag	tggattagaa	tcaaactggg	acattgatcc	acttgagccg											737
ttaagtgtg	ccaattgtac	aatatgccc	ggcttgcaga	ataaagccaa	ctttttattg											797
tgaataataa	taaggacata	tttttcttca	gattatgttt	tatttctttg	cattgagtga											857
ggtacataaa	atggcttggt	aaaagtaata	aatcagtag	aatcactaac	tttcctttgt											917
acatattatt	ttgcagtata	gatgaatatt	actaatcagt	ttgattattc	tcagaggggtg											977
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taaccaatca	gtgtttttaat	gtttgtgtgt	tcttcataaa	atttaaatac	aattcgttat											1097
tctgtttcca	atgttagtat	gtatgtaaac	atgatagtag	agccattttt	ttcatatgtg											1157
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<212> DNA

<213> Homo sapiens

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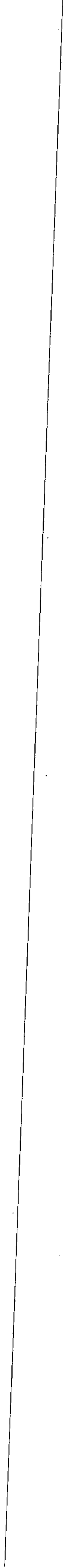
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<222> 36..107


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<222> 1389..1400
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                               Met Ala Ser Leu Gly Leu
                               -20
caa ctt gtg ggc tac atc cta ggc ctt ctg ggg ctt ttg ggc aca ctg      101
Gln Leu Val Gly Tyr Ile Leu Gly Leu Leu Gly Leu Leu Gly Thr Leu
      -15                               -10                               -5
gtt gcc atg ctg ctc ccc agc tgg aaa aca agt tct tat gtc ggt gcc      149
Val Ala Met Leu Leu Pro Ser Trp Lys Thr Ser Ser Tyr Val Gly Ala
      1                               5                               10
agc att gtg aca gca gtt ggc ttc tcc aag ggc ctc tgg atg gaa tgt      197
Ser Ile Val Thr Ala Val Gly Phe Ser Lys Gly Leu Trp Met Glu Cys
      15                               20                               25                               30
gcc aca cac agc aca ggc atc acc cag tgt gac atc tat agc acc ctt      245
Ala Thr His Ser Thr Gly Ile Thr Gln Cys Asp Ile Tyr Ser Thr Leu
      35                               40                               45
ctg ggc ctg ccc gct gac atc cag gct gcc cag gcc atg atg gtg aca      293
Leu Gly Leu Pro Ala Asp Ile Gln Ala Ala Gln Ala Met Met Val Thr
      50                               55                               60
tcc agt gca atc tcc tcc ctg gcc tgc att atc tct gtg gtg ggc atg      341
Ser Ser Ala Ile Ser Ser Leu Ala Cys Ile Ile Ser Val Val Gly Met
      65                               70                               75
aga tgc aca gtc ttc tgc cag gaa tcc cga gcc aaa gac aga gtg gcg      389
Arg Cys Thr Val Phe Cys Gln Glu Ser Arg Ala Lys Asp Arg Val Ala
      80                               85                               90
gta gca ggt gga gtc ttt ttc atc ctt gga ggc ctc ctg gga ttc att      437
Val Ala Gly Gly Val Phe Phe Ile Leu Gly Gly Leu Leu Gly Phe Ile
      95                               100                               105                               110
cct gtt gcc tgg aat ctt cat ggg atc cta cgg gac ttc tac tca cca      485
Pro Val Ala Trp Asn Leu His Gly Ile Leu Arg Asp Phe Tyr Ser Pro
      115                               120                               125
ctg gtg cct gac agc atg aaa ttt gag att gga gag gct ctt tac ttg      533
Leu Val Pro Asp Ser Met Lys Phe Glu Ile Gly Glu Ala Leu Tyr Leu
      130                               135                               140
ggc att att tct tcc ctg ttc tcc ctg ata gct gga atc atc ctc tgc      581
Gly Ile Ile Ser Ser Leu Phe Ser Leu Ile Ala Gly Ile Ile Leu Cys
      145                               150                               155
ttt tcc tgc tca tcc cag aga aat cgc tcc aac tac tac gat gcc tac      629
Phe Ser Cys Ser Ser Gln Arg Asn Arg Ser Asn Tyr Tyr Asp Ala Tyr
      160                               165                               170
caa gcc caa cct ctt gcc aca agg agc tct cca agg cct ggt caa cct      677
Gln Ala Gln Pro Leu Ala Thr Arg Ser Ser Pro Arg Pro Gly Gln Pro
      175                               180                               185                               190
ccc aaa gtc aag agt gag ttc aat tcc tac agc ctg aca ggg tat gtg      725
Pro Lys Val Lys Ser Glu Phe Asn Ser Tyr Ser Leu Thr Gly Tyr Val
      195                               200                               205
tgaagaacca ggggccagag ctgggggggtg gctgggtctg tgaaaaacag tggacagcac      785
cccgagggcc acaggtgagg gacactacca ctggatcgtg tcagaagggtg ctgctgaggg      845
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tgcttttagta gtagtttaaa gtagtaactg ctactgtatt tagtgggggtg gaattcagaa      120
gaaatttgaa gaccagatca tgggtggtct gcatgtgaat gaacagga atg agc cag      177
                                         Met Ser Gln
aca gcc tgg ctg tca ttg ctt tct tcc tcc cca ttt gga ccc ttc tct      225
Thr Ala Trp Leu Ser Leu Leu Ser Ser Ser Pro Phe Gly Pro Phe Ser
-30                               -25                               -20                               -15
gcc ctt aca ttt ttg ttt ctc cat cta cca cca tcc acc agt cta ttt      273
Ala Leu Thr Phe Leu Phe Leu His Leu Pro Pro Ser Thr Ser Leu Phe
                               -10                               -5                               1
att aac tta gca aga gga caa ata aag ggc cct ctt ggc ttg att ttg      321
Ile Asn Leu Ala Arg Gly Gln Ile Lys Gly Pro Leu Gly Leu Ile Leu
                               5                               10                               15
ctt ctt tct ttc tgt gga gga tat act aag tgc gac ttt gcc cta tcc      369
Leu Leu Ser Phe Cys Gly Gly Tyr Thr Lys Cys Asp Phe Ala Leu Ser
                               20                               25                               30
tat ttg gaa atc cct aac aga att gag ttt tct att atg gat cca aaa      417
Tyr Leu Glu Ile Pro Asn Arg Ile Glu Phe Ser Ile Met Asp Pro Lys
35                               40                               45                               50
aga aaa aca aaa tgc taatgaagcc atcagtcaag ggtcacatgc caataaaca      472
Arg Lys Thr Lys Cys
                               55
taaattttcc agaagaaatg aaatccaact agacaaataa agtagagctt atgaaatggt      532
tcagtaagga tgagcttggt gttttttggt ttgttttggt ttgttttttt aaagacggag      592
tctcgctctg tcaactcaggc tggagtgcag tggatatgatc ttggctcact gtaacctccg      652
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gtgccaccat gcctggctaa tttttgtggt tttggtagag acaggggttc accacgttgg      772
tcgggctggt ctcggtctcc tgacctcttg atccgcctgc cttggcctcc caaagtgatg      832
ggattacaga tgtgagccac cgtgcctagc caaggatgag attttttaaag tatgttccag      892
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<222> 143..238
<223> Von Heijne matrix
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<222> 697..702
<220>

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<221> polyA_site
<222> 721..730
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<222> 1,14,28,52
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gagccgatgg aagagttcac tc atg ttt gca ccc gcg gtg acg cgt gct ttt      172
                Met Phe Ala Pro Ala Val Thr Arg Ala Phe
                        -30                        -25
cgc aag aac aag act ctc ggc tat gga gtc ccc atg ttg ttg ctg att      220
Arg Lys Asn Lys Thr Leu Gly Tyr Gly Val Pro Met Leu Leu Leu Ile
        -20                        -15                        -10
gtt gga ggt tct ttt ggt ctt cgt gag ttt tct caa atc cga tat gat      268
Val Gly Gly Ser Phe Gly Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp
        -5                        1                        5                        10
gct gtg aag agt aaa atg gat cct gag ctt gaa aaa aaa ctg aaa gag      316
Ala Val Lys Ser Lys Met Asp Pro Glu Leu Glu Lys Lys Leu Lys Glu
        15                        20                        25
aat aaa ata tct tta gag tcg gaa tat gag aaa atc aaa gac tcc aag      364
Asn Lys Ile Ser Leu Glu Ser Glu Tyr Glu Lys Ile Lys Asp Ser Lys
        30                        35                        40
ttt gat gac tgg aag aat att cga gga ccc agg cct tgg gaa gat cct      412
Phe Asp Asp Trp Lys Asn Ile Arg Gly Pro Arg Pro Trp Glu Asp Pro
        45                        50                        55
gac ctc ctc caa gga aga aat cca gaa agc ctt aag act aag aca act      460
Asp Leu Leu Gln Gly Arg Asn Pro Glu Ser Leu Lys Thr Lys Thr Thr
        60                        65                        70
tgactctgct gattctcttt tccttttttt ttttaaataa aaatactatt aactggactt      520
cctaatatat acttctatca agtggaaagg aaattccagg cccatggaaa cttggatatg      580
ggtaatttga tgacaaataa tcttcactaa aggtcatgta cagggttttta tacttcccag      640
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aaaaatgtga atactgtctc aaaaaaaaaa      730

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tgaagactaa cattttgtga agttgtataaa cagaaaacct gttagaa atg tgg tgg      116
                                Met Trp Trp
                                -20
ttt cag caa ggc ctc agt ttc ctt cct tca gcc ctt gta att tgg aca      164

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100

Phe	Gln	Gln	Gly	Leu	Ser	Phe	Leu	Pro	Ser	Ala	Leu	Val	Ile	Trp	Thr									
			-15					-10					-5											
tct	gct	gct	ttc	ata	ttt	tca	tac	att	act	gca	gta	aca	ctc	cac	cat	212								
Ser	Ala	Ala	Phe	Ile	Phe	Ser	Tyr	Ile	Thr	Ala	Val	Thr	Leu	His	His									
		1				5					10													
ata	gac	ccg	gct	tta	cct	tat	atc	agt	gac	act	ggg	aca	gta	gct	cca	260								
Ile	Asp	Pro	Ala	Leu	Pro	Tyr	Ile	Ser	Asp	Thr	Gly	Thr	Val	Ala	Pro									
15					20				25					30										
gaa	aaa	tgc	tta	ttt	ggg	gca	atg	cta	aat	att	gcg	gca	gtt	tta	tgc	308								
Glu	Lys	Cys	Leu	Phe	Gly	Ala	Met	Leu	Asn	Ile	Ala	Ala	Val	Leu	Cys									
			35			40							45											
att	gct	acc	att	tat	gtt	cgt	tat	aag	caa	gtt	cat	gct	ctg	agt	cct	356								
Ile	Ala	Thr	Ile	Tyr	Val	Arg	Tyr	Lys	Gln	Val	His	Ala	Leu	Ser	Pro									
			50			55							60											
gaa	gag	aac	gtt	atc	atc	aaa	tta	aac	aag	gct	ggc	ctt	gta	ctt	gga	404								
Glu	Glu	Asn	Val	Ile	Ile	Lys	Leu	Asn	Lys	Ala	Gly	Leu	Val	Leu	Gly									
		65				70					75													
ata	ctg	agt	tgt	tta	gga	ctt	tct	att	gtg	gca	aac	ttc	cag	aaa	aca	452								
Ile	Leu	Ser	Cys	Leu	Gly	Leu	Ser	Ile	Val	Ala	Asn	Phe	Gln	Lys	Thr									
	80				85						90													
acc	ctt	ttt	gct	gca	cat	gta	agt	gga	gct	gtg	ctt	acc	ttt	ggg	atg	500								
Thr	Leu	Phe	Ala	Ala	His	Val	Ser	Gly	Ala	Val	Leu	Thr	Phe	Gly	Met									
95					100					105					110									
ggc	tca	tta	tat	atg	ttt	gtt	cag	acc	atc	ctt	tcc	tac	caa	atg	cag	548								
Gly	Ser	Leu	Tyr	Met	Phe	Val	Gln	Thr	Ile	Leu	Ser	Tyr	Gln	Met	Gln									
			115			120							125											
ccc	aaa	atc	cat	ggc	aaa	caa	gtc	ttc	tgg	atc	aga	ctg	ttg	ttg	gtt	596								
Pro	Lys	Ile	His	Gly	Lys	Gln	Val	Phe	Trp	Ile	Arg	Leu	Leu	Leu	Val									
			130			135						140												
atc	tgg	tgt	gga	gta	agt	gca	ctt	agc	atg	ctg	act	tgc	tca	tca	gtt	644								
Ile	Trp	Cys	Gly	Val	Ser	Ala	Leu	Ser	Met	Leu	Thr	Cys	Ser	Ser	Val									
		145				150						155												
ttg	cac	agt	ggc	aat	ttt	ggg	act	gat	tta	gaa	cag	aaa	ctc	cat	tgg	692								
Leu	His	Ser	Gly	Asn	Phe	Gly	Thr	Asp	Leu	Glu	Gln	Lys	Leu	His	Trp									
	160				165						170													
aac	ccc	gag	gac	aaa	ggg	tat	gcg	ctt	cac	atg	atc	act	act	gca	gca	740								
Asn	Pro	Glu	Asp	Lys	Gly	Tyr	Ala	Leu	His	Met	Ile	Thr	Thr	Ala	Ala									
175					180					185					190									
gaa	tgg	tct	atg	tca	ttt	tcc	ttc	ttt	ggg	ttt	ttc	ctg	act	tac	att	788								
Glu	Trp	Ser	Met	Ser	Phe	Ser	Phe	Phe	Gly	Phe	Phe	Leu	Thr	Tyr	Ile									
			195			200						205												
cgt	gat	ttt	cag	aaa	att	tcc	tta	cgg	gtg	gaa	gcc	aac	tta	cat	gga	836								
Arg	Asp	Phe	Gln	Lys	Ile	Ser	Leu	Arg	Val	Glu	Ala	Asn	Leu	His	Gly									
			210			215						220												
tta	acc	ctc	tat	gac	act	gca	cct	tgc	cct	att	aac	aat	gaa	cga	aca	884								
Leu	Thr	Leu	Tyr	Asp	Thr	Ala	Pro	Cys	Pro	Ile	Asn	Asn	Glu	Arg	Thr									
		225				230					235													
cgg	cta	ctt	tcc	aga	gat	att	aga	tgaaaggata aaatatttct gtaatgatta								938								
Arg	Leu	Leu	Ser	Arg	Asp	Ile	Arg																	
	240				245																			
tgattctcag ggattgggga aagggttcaca gaagttgctt attcttctct gaaattttca																998								
accacttaat caaggctgac agtaacactg atgaatgctg ataatcagga aacatgaaag																1058								
aagccatttg atagattatt ctaaaggata tcatcaagaa gactattaaa aacacctatg																1118								
cctatacttt tttatctcag aaaataaagt caaaagacta tgaaaaaaa aaaaaa																1174								

<210> 144
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1234567890
1234567890
1234567890

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<222> 652
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tcttcatctt ggatttgaaa gttgagagca gcatgttttg cccactgaaa ctcacctgcs      120
tgrsagtgtg mtggattatt ccttgggcct gaatgacttg aatgtttccc cgcctgagct      180
aacagtcctat gtgggtgatt cagctctg atg gga tgt gtt ttc cag agc aca      232
                               Met Gly Cys Val Phe Gln Ser Thr
                               1               5
gaa gac aaa tgt ata ttc aag ata gac tgg act ctg tca cca gga gag      280
Glu Asp Lys Cys Ile Phe Lys Ile Asp Trp Thr Leu Ser Pro Gly Glu
    10               15               20
cac gcc aag gac gaa tat gtg cta tac tat tac tcc aat ctc agt gtg      328
His Ala Lys Asp Glu Tyr Val Leu Tyr Tyr Tyr Ser Asn Leu Ser Val
    25               30               35               40
cct att ggg cgc ttc cag aac cgc gta cac ttg atg ggg gac atc tta      376
Pro Ile Gly Arg Phe Gln Asn Arg Val His Leu Met Gly Asp Ile Leu
    45               50               55
tgc aat gat ggc tct ctc ctg ctc caa gat gtg caa gag gct gac cag      424
Cys Asn Asp Gly Ser Leu Leu Leu Gln Asp Val Gln Glu Ala Asp Gln
    60               65               70
gga acc tat atc tgt gaa atc cgc ctc aaa ggg gag agc cag gtg ttc      472
Gly Thr Tyr Ile Cys Glu Ile Arg Leu Lys Gly Glu Ser Gln Val Phe
    75               80               85
aag aag gcg gtg gta ctg cat gtg ctt cca gag gag ccc aaa ggt acg      520
Lys Lys Ala Val Val Leu His Val Leu Pro Glu Glu Pro Lys Gly Thr
    90               95               100
caa atg ctt act taaagagggg ccaaggggca agagctttca tgtgcaagag      572
Gln Met Leu Thr
105
gcaaggaaac tgattatctt gagtaaagtc cagccttttg gctaagtact taccacagag      632
tgaatcttca aagaaatgan tcattaaatt atttcagrtc agaataaaaa takgagttat      692
tttagttaak aataaaatat tgataattat tgtattatta ctttaaacac acttccccct      752
cacaaaagcc ctgtgaagga tgttttgttc acatataatg tccaaatatg ttttggacac      812
atatttatta aatggaataa atagtamtg aaccctggca ccthtgacaa caaagtcyat      872
gttyttttta ctatgccta atacctttsa tcagttatcc acattgatgc tacatytgta      932
ttttataggt accctatgtt aggtgttttg ggggatagaa aagaaataag cagkycaggc      992
tcagtggctc atgcctgtaa tcctagcatt ttgggaggct gaggcagcag aamtgcctga     1052
gccccagggt tcaagactgc agtgagctat gawggcacca ctgcattyta gcctgggwga     1112
cagagcaaga ctytgtttaa aataaaaaaa gagaaaaaaa aaaaaa                    1158

<210> 145
<211> 754
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 5..142
<223> Von Heijne matrix

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score 6.59999990463257
seq VCCYLFWLIAILA/QL
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<222> 716..721
<220>
<221> polyA_site
<222> 742..754
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    Met Ser Val Phe Trp Gly Phe Val Gly Phe Leu Val Pro Trp Phe
        -45                      -40                      -35
atc ccc aag ggt cct aac cgg gga gtt atc att acc atg ttg gtg acc      97
Ile Pro Lys Gly Pro Asn Arg Gly Val Ile Ile Thr Met Leu Val Thr
    -30                      -25                      -20
tgt tca gtt tgc tgc tat ctc ttt tgg ctg att gca att ctg gcc caa      145
Cys Ser Val Cys Cys Tyr Leu Phe Trp Leu Ile Ala Ile Leu Ala Gln
    -15                      -10                      -5                      1
ctc aac cct ctc ttt gga ccg caa ttg aaa aat gaa acc atc tgg tat      193
Leu Asn Pro Leu Phe Gly Pro Gln Leu Lys Asn Glu Thr Ile Trp Tyr
        5                      10                      15
ctg aag tat cat tgg cct tgaggaagaa gacatgctct acagtgtctca      241
Leu Lys Tyr His Trp Pro
    20
gtcttttgagg tcacgagaag agaatgcctt ctagatgcaa aatcacctct aaaccagacc      301
acttttcttg acttgccctgt tttggccatt agctgcctta aacgttaaca gcacatttga      361
atgccttatt ctacaatgca gcgtgttttc ctttgccttt tttgcacttt ggtgaattac      421
gtgcctccat aacctgaact gtgccgactc cacaaaacga ttatgtactc ttctgagata      481
gaagatgctg ttcttctgag agatacgtta ctctctcctt ggaatctgtg gatttgaaga      541
tggctcctgc cttctcacgt gggaatcagt gaagtgttta gaaactgctg caagacaaac      601
aagactccag tggggtggtc agtaggagag cacgttcaga gggaagagcc atctcaacag      661
aatcgcacca aactatactt tcaggatgaa tttcttcttt ctgccatctt ttggaataaa      721
tattttcttc ctttctatgt aaaaaaaaaa aaa      754

<210> 146
<211> 1073
<212> DNA
<213> Homo sapiens
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<221> sig_peptide
<222> 98..181
<223> Von Heijne matrix
score 3.59999990463257
seq PLSDSWALLPASA/GV
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<221> polyA_signal
<222> 1035..1040
<220>
<221> polyA_site
<222> 1060..1073
<400> 146
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cgctggggga gctccgcgcc gccggacgcc cgtgacc atg tgg agg ctg ctg gct      115
                                Met Trp Arg Leu Leu Ala
                                    -25
cgc gct agt gcg ccg ctc ctg cgg gtg ccc ttg tca gat tcc tgg gca      163
Arg Ala Ser Ala Pro Leu Leu Arg Val Pro Leu Ser Asp Ser Trp Ala
    -20                      -15                      -10

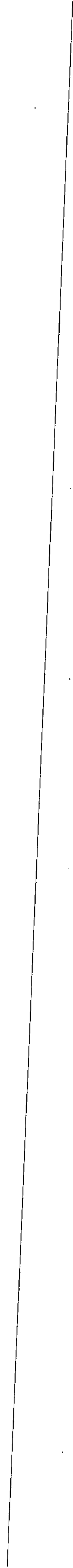
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287



ctc ctc ccc gcc agt gct ggc gta aag aca ctg ctc cca gta cca agt	211
Leu Leu Pro Ala Ser Ala Gly Val Lys Thr Leu Leu Pro Val Pro Ser	
-5 1 5 10	
ttt gaa gat gtt tcc att cct gaa aaa ccc aag ctt aga ttt att gaa	259
Phe Glu Asp Val Ser Ile Pro Glu Lys Pro Lys Leu Arg Phe Ile Glu	
15 20 25	
agg gca cca ctt gtg cca aaa gta aga aga gaa cct aaa aat tta agt	307
Arg Ala Pro Leu Val Pro Lys Val Arg Arg Glu Pro Lys Asn Leu Ser	
30 35 40	
gac ata cgg gga cct tcc act gaa gct acg gag ttt aca gaa ggc aat	355
Asp Ile Arg Gly Pro Ser Thr Glu Ala Thr Glu Phe Thr Glu Gly Asn	
45 50 55	
ttt gca atc ttg gca ttg ggt ggt ggc tac ctg cat tgg ggc cac ttt	403
Phe Ala Ile Leu Ala Leu Gly Gly Gly Tyr Leu His Trp Gly His Phe	
60 65 70	
gaa atg atg cgc ctg aca atc aac cgc tct atg gac ccc aag aac atg	451
Glu Met Met Arg Leu Thr Ile Asn Arg Ser Met Asp Pro Lys Asn Met	
75 80 85 90	
ttt gcc ata tgg cga gta cca gcc cct ttc aag ccc atc act cgc aaa	499
Phe Ala Ile Trp Arg Val Pro Ala Pro Phe Lys Pro Ile Thr Arg Lys	
95 100 105	
agt gtt ggg cat cgc atg ggg gga ggc aaa ggt gct att gac cac tac	547
Ser Val Gly His Arg Met Gly Gly Gly Lys Gly Ala Ile Asp His Tyr	
110 115 120	
gtg aca cct gtg aag gct ggc cgc ctt gtt gta gag atg ggt ggg cgt	595
Val Thr Pro Val Lys Ala Gly Arg Leu Val Val Glu Met Gly Gly Arg	
125 130 135	
tgt gaa ttt gaa gaa gtg caa ggt ttc ctt gac cag gtt gcc cac aag	643
Cys Glu Phe Glu Glu Val Gln Gly Phe Leu Asp Gln Val Ala His Lys	
140 145 150	
ttg ccc ttc gca gca aag gct gtg agc cgc ggg act cta gag aag atg	691
Leu Pro Phe Ala Ala Lys Ala Val Ser Arg Gly Thr Leu Glu Lys Met	
155 160 165 170	
cga aaa gat caa gag gaa aga gaa cgt aac aac cag aac ccc tgg aca	739
Arg Lys Asp Gln Glu Glu Arg Glu Arg Asn Asn Gln Asn Pro Trp Thr	
175 180 185	
ttt gag cga ata gcc act gcc aac atg ctg ggc ata cgg aaa gta ctg	787
Phe Glu Arg Ile Ala Thr Ala Asn Met Leu Gly Ile Arg Lys Val Leu	
190 195 200	
agc cca tat gac ttg acc cac aag ggg aaa tac tgg ggc aag ttc tac	835
Ser Pro Tyr Asp Leu Thr His Lys Gly Lys Tyr Trp Gly Lys Phe Tyr	
205 210 215	
atg ccc aaa cgt gtg tagtgagtgt aggagataac tgtatatagg ctactgaaag	890
Met Pro Lys Arg Val	
220	
aaggattctg catttctatt ccctcagcc taccactga agtctttggg tagctcttaa	950
gccataacta aggagcagca tttgagtaga tttctgaaaa acgatgttat ttgttgattt	1010
aaaaagaaaa ctgtattttt attaaataaa atttaaacad cacttcagga aaaaaaaaaa	1070
aaa	1073

<210> 147
 <211> 413
 <212> DNA
 <213> Homo sapiens
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 <222> 46..189
 <223> Von Heijne matrix



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score 4.09999990463257
seq VFMLIVSVLALIP/ET
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<222> 377..382
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<221> polyA_site
<222> 402..413
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                                         Met Asp Asn Val
                                         -45

cag ccg aaa ata aaa cat cgc ccc ttc tgc ttc agt gtg aaa ggc cac      105
Gln Pro Lys Ile Lys His Arg Pro Phe Cys Phe Ser Val Lys Gly His
                    -40                    -35                    -30

gtg aag atg ctg cgg ctg gat att atc aac tca ctg gta aca aca gta      153
Val Lys Met Leu Arg Leu Asp Ile Ile Asn Ser Leu Val Thr Thr Val
                    -25                    -20                    -15

ttc atg ctc atc gta tct gtg ttg gca ctg ata cca gaa acc aca aca      201
Phe Met Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu Thr Thr Thr
                    -10                    -5                    1

ttg aca gtt ggt gga ggg gtg ttt gca ctt gtg aca gca gta tgc tgc      249
Leu Thr Val Gly Gly Gly Val Phe Ala Leu Val Thr Ala Val Cys Cys
5                    10                    15                    20

ctt gcc gac ggg gcc ctt att tac cgg aag ctt ctg ttc aat ccc agc      297
Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe Asn Pro Ser
                    25                    30                    35

ggg cct tac cag aaa aag cct gtg cat gaa aaa aaa gaa gtt ttg      342
Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu Val Leu
                    40                    45                    50

taattttata ttacttttta gtttgatact aagtattaaa catatttctg tattcttcca      402
aaaaaaaaaa a      413

<210> 148
<211> 609
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 139..231
<223> Von Heijne matrix
score 4.40000009536743
seq TCCHLGLPHPVRA/PR
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<221> polyA_signal
<222> 579..584
<220>
<221> polyA_site
<222> 598..609
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tcaatgagat tgaacttcag ctggattgaa agagaggcta gaagttccgc ttgccagcag      120
cctccttagt agagcgga atg agt aat acc cac acg gtg ctt gtc tca ctt      171
                                         Met Ser Asn Thr His Thr Val Leu Val Ser Leu
                                         -30                    -25

ccc cat ccg cac ccg gcc ctc acc tgc tgt cac ctc ggc ctc cca cac      219
Pro His Pro His Pro Ala Leu Thr Cys Cys His Leu Gly Leu Pro His
-20                    -15                    -10                    -5

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ccg gtc cgc gct ccc cgc cct ctt cct cgc gta gaa ccg tgg gat cct	267
Pro Val Arg Ala Pro Arg Pro Leu Pro Arg Val Glu Pro Trp Asp Pro	
1 5 10	
agg tgg cag gac tca gag cta agg tat cca cag gcc atg aat tcc ttc	315
Arg Trp Gln Asp Ser Glu Leu Arg Tyr Pro Gln Ala Met Asn Ser Phe	
15 20 25	
cta aat gag cgg tca tcg ccg tgc agg acc tta agg caa gaa gca tcg	363
Leu Asn Glu Arg Ser Ser Pro Cys Arg Thr Leu Arg Gln Glu Ala Ser	
30 35 40	
gct gac aga tgt gat ctc tgaacctgat agattgctga ttttatctta	411
Ala Asp Arg Cys Asp Leu	
45 50	
ttttatcctt gacttggtac aagttttggg atttctgaaa agaccataca gataaccaca	471
aatatcaaga aagtcgtctt cagtattaag tagaatttag atttaggttt ccttcctgct	531
tcccacctcc ttcgaataag gaaacgtctt tgggaccaac tttatggaat aaataagctg	591
agctgcaaaa aaaaaaaaa	609

<210> 149

<211> 522

<212> DNA

<213> Homo sapiens

<220>

<221> polyA_site

<222> 512..522

<220>

<221> misc_feature

<222> 11

<223> n=a, g, c or t

<400> 149

ccaactgcag ntctgaattt accgagcggg gaggagatgc acacggcact cgagtgtgag	60
gaaaaataga a atg aag gta cat atg cac aca aaa ttt tgc ctc att tgt	110
Met Lys Val His Met His Thr Lys Phe Cys Leu Ile Cys	
1 5 10	
ttg ctg aca ttt att ttt cat cat tgc aac cat tgc cat gaa gaa cat	158
Leu Leu Thr Phe Ile Phe His His Cys Asn His Cys His Glu Glu His	
15 20 25	
gac cat ggc cct gaa gcg ctt cac aga cag cat cgt gga atg aca gaa	206
Asp His Gly Pro Glu Ala Leu His Arg Gln His Arg Gly Met Thr Glu	
30 35 40 45	
ttg gag cca agc aaa ttt tca aag caa gct gct gaa aat gaa aaa aaa	254
Leu Glu Pro Ser Lys Phe Ser Lys Gln Ala Ala Glu Asn Glu Lys Lys	
50 55 60	
tac tat att gaa aaa ctt ttt gag cgt tat ggt gaa aat gga aga tta	302
Tyr Tyr Ile Glu Lys Leu Phe Glu Arg Tyr Gly Glu Asn Gly Arg Leu	
65 70 75	
tcc ttt ttt ggt ttg gag aaa ctt tta aca aac ttg ggc ctt gga gag	350
Ser Phe Phe Gly Leu Glu Lys Leu Leu Thr Asn Leu Gly Leu Gly Glu	
80 85 90	
aga aaa gta gtt gag att aat cat gag gat ctt ggc cac gat cat gtt	398
Arg Lys Val Val Glu Ile Asn His Glu Asp Leu Gly His Asp His Val	
95 100 105	
tct cat tta ggt att ttg gca gtt.caa gag gga aag cat ttt cac tca	446
Ser His Leu Gly Ile Leu Ala Val Gln Glu Gly Lys His Phe His Ser	
110 115 120 125	
cat aac cac cag cat tcc cat aat cat tta aat tca gaa aat caa act	494
His Asn His Gln His Ser His Asn His Leu Asn Ser Glu Asn Gln Thr	
130 135 140	
gtg acc agt gta tcc aca aaaaaaaaa	522

290

Val Thr Ser Val Ser Thr
145

<210> 150

<211> 1322

<212> DNA

<213> Homo sapiens

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<221> sig_peptide

<222> 126..260

<223> Von Heijne matrix

score 4.59999990463257

seq VLVYLVTAERVWS/DD

<220>

<221> polyA_signal

<222> 1283..1288

<220>

<221> polyA_site

<222> 1309..1322

<400> 150

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gctgctggga gccaggagag ccctgaggag tagtcactca gtagcagctg acgcgtgggt	120
ccacc atg aac tgg agt atc ttt gag gga ctc ctg agt ggg gtc aac aag	170
Met Asn Trp Ser Ile Phe Glu Gly Leu Leu Ser Gly Val Asn Lys	
-45 -40 -35	
tac tcc aca gcc ttt ggg cgc atc tgg ctg tct ctg gtc ttc atc ttc	218
Tyr Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe Ile Phe	
-30 -25 -20 -15	
cgc gtg ctg gtg tac ctg gtg acg gcc gag cgt gtg tgg agt gat gac	266
Arg Val Leu Val Tyr Leu Val Thr Ala Glu Arg Val Trp Ser Asp Asp	
-10 -5 1	
cac aag gac ttc gac tgc aat act cgc cag ccc ggc tgc tcc aac gtc	314
His Lys Asp Phe Asp Cys Asn Thr Arg Gln Pro Gly Cys Ser Asn Val	
5 10 15	
tgc ttt gat gag ttc ttc cct gtg tcc cat gtg cgc ctc tgg gcc ctg	362
Cys Phe Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu	
20 25 30	
cag ctt atc ctg gtg aca tgc ccc tca ctg ctc gtg gtc atg cac gtg	410
Gln Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val	
35 40 45 50	
gcc tac cgg gag gtt cag gag aag agg cac cga gaa gcc cat ggg gag	458
Ala Tyr Arg Glu Val Gln Glu Lys Arg His Arg Glu Ala His Gly Glu	
55 60 65	
aac agt ggg cgc ctc tac ctg aac ccc ggc aag aag cgg ggt ggg ctc	506
Asn Ser Gly Arg Leu Tyr Leu Asn Pro Gly Lys Lys Arg Gly Gly Leu	
70 75 80	
tgg tgg aca tat gtc tgc agc cta gtg ttc aag gcg agc gtg gac atc	554
Trp Trp Thr Tyr Val Cys Ser Leu Val Phe Lys Ala Ser Val Asp Ile	
85 90 95	
gcc ttt ctc tat gtg ttc cac tca ttc tac ccc aaa tat atc ctc cct	602
Ala Phe Leu Tyr Val Phe His Ser Phe Tyr Pro Lys Tyr Ile Leu Pro	
100 105 110	
cct gtg gtc aag tgc cac gca gat cca tgt ccc aat ata gtg gac tgc	650
Pro Val Val Lys Cys His Ala Asp Pro Cys Pro Asn Ile Val Asp Cys	
115 120 125 130	
ttc atc tcc aag ccc tca gag aag aac att ttc acc ctc ttc atg gtg	698
Phe Ile Ser Lys Pro Ser Glu Lys Asn Ile Phe Thr Leu Phe Met Val	
135 140 145	

291

gcc aca gct gcc atc tgc atc ctg ctc aac ctc gtg gag ctc atc tac	746
Ala Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Val Glu Leu Ile Tyr	
150 155 160	
ctg gtg agc aag aga tgc cac gag tgc ctg gca gca agg aaa gct caa	794
Leu Val Ser Lys Arg Cys His Glu Cys Leu Ala Ala Arg Lys Ala Gln	
165 170 175	
gcc atg tgc aca ggt cat cac ccc cac gat acc acc tct tcc tgc aaa	842
Ala Met Cys Thr Gly His His Pro His Asp Thr Thr Ser Ser Cys Lys	
180 185 190	
caa gac gac ctc ctt tgc ggt gac ctc atc ttt ctg ggc tca gac agt	890
Gln Asp Asp Leu Leu Ser Gly Asp Leu Ile Phe Leu Gly Ser Asp Ser	
195 200 205 210	
cat cct cct ctc tta cca gac cgc ccc cga gac cat gtg aag aaa acc	938
His Pro Pro Leu Leu Pro Asp Arg Pro Arg Asp His Val Lys Lys Thr	
215 220 225	
atc ttg tgaggggctg cctggactgg tctggcaggt tgggcctgga tggggaggct	994
Ile Leu	
ctagcatctc tcataggtgc aacctgagag tgggggagct aagccatgag gtaggggcag	1054
gcaagagaga ggattcagac gctctgggag ccagttccta gtcctcaact ccagccacct	1114
gccccagctc gacggcactg ggccagttcc ccctctgctc tgcagctcgg tttccttttc	1174
tagaatggaa atagtgaggg ccaatgccca gggttggagg gaggagggcg ttcatagaag	1234
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Met Ala Ser	
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aaa atc ttg ctt aac gta caa gag gag gtg acc tgt ccc atc tgc ctg	106
Lys Ile Leu Leu Asn Val Gln Glu Glu Val Thr Cys Pro Ile Cys Leu	
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gag ctg ttg aca gaa ccc ttg agt cta gac tgt ggc cac agc ctc tgc	154
Glu Leu Leu Thr Glu Pro Leu Ser Leu Asp Cys Gly His Ser Leu Cys	
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cga gcc tgc atc act gtg agc aac aag gag gca gtg acc agc atg gga	202
Arg Ala Cys Ile Thr Val Ser Asn Lys Glu Ala Val Thr Ser Met Gly	
1 5 10	
gga aaa agc agc tgt cct gtg tgt ggt atc agt tac tca ttt gaa cat	250
Gly Lys Ser Ser Cys Pro Val Cys Gly Ile Ser Tyr Ser Phe Glu His	
15 20 25 30	
cta cag gct aat cag cat ctg gcc aac ata gtg gag aga ctc aag gag	298
Leu Gln Ala Asn Gln His Leu Ala Asn Ile Val Glu Arg Leu Lys Glu	
35 40 45	
gtc aag ttg agc cca gac aat ggg aag aag aga gat ctc tgt gat cat	346
Val Lys Leu Ser Pro Asp Asn Gly Lys Lys Arg Asp Leu Cys Asp His	



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1000

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His	Gly	Glu	Lys	Leu	Leu	Leu	Phe	Cys	Lys	Glu	Asp	Arg	Lys	Val	Ile				
		65					70					75							
tgc	tgg	ctt	tgt	gag	cgg	tct	cag	gag	cac	cgt	ggt	cac	cac	aca	gtc		442		
Cys	Trp	Leu	Cys	Glu	Arg	Ser	Gln	Glu	His	Arg	Gly	His	His	Thr	Val				
	80					85					90								
ctc	acg	gag	gaa	gta	ttc	aag	gaa	tgt	cag	gag	aaa	ctc	cag	gca	gtc		490		
Leu	Thr	Glu	Glu	Val	Phe	Lys	Glu	Cys	Gln	Glu	Lys	Leu	Gln	Ala	Val				
95					100					105					110				
ctc	aag	agg	ctg	aag	aag	gaa	gag	gag	gaa	gct	gag	aag	ctg	gaa	gct		538		
Leu	Lys	Arg	Leu	Lys	Lys	Glu	Glu	Glu	Glu	Ala	Glu	Lys	Leu	Glu	Ala				
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Asp	Ile	Arg	Glu	Glu	Lys	Thr	Ser	Trp	Lys	Tyr	Gln	Val	Gln	Thr	Glu				
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aga	caa	agg	ata	caa	aca	gaa	ttt	gat	cag	ctt	aga	agc	atc	cta	aat		634		
Arg	Gln	Arg	Ile	Gln	Thr	Glu	Phe	Asp	Gln	Leu	Arg	Ser	Ile	Leu	Asn				
		145					150					155							
aat	gag	gag	cag	aga	gag	ctg	caa	aga	ttg	gaa	gaa	gaa	gaa	aag	aag		682		
Asn	Glu	Glu	Gln	Arg	Glu	Leu	Gln	Arg	Leu	Glu	Glu	Glu	Glu	Lys	Lys				
	160					165				170									
acg	ctg	gat	aag	ttt	gca	gag	gct	gag	gat	gag	cta	gtt	cag	cag	aag		730		
Thr	Leu	Asp	Lys	Phe	Ala	Glu	Ala	Glu	Asp	Glu	Leu	Val	Gln	Gln	Lys				
175					180					185					190				
cag	ttg	gtg	aga	gag	ctc	atc	tca	gat	gtg	gag	tgt	cgg	agt	cag	tgg		778		
Gln	Leu	Val	Arg	Glu	Leu	Ile	Ser	Asp	Val	Glu	Cys	Arg	Ser	Gln	Trp				
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tca	aca	atg	gag	ctg	ctg	cag	gac	atg	agt	gga	atc	atg	aaa	tgg	agt		826		
Ser	Thr	Met	Glu	Leu	Leu	Gln	Asp	Met	Ser	Gly	Ile	Met	Lys	Trp	Ser				
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Glu	Ile	Trp	Arg	Leu	Lys	Lys	Pro	Lys	Met	Val	Ser	Lys	Lys	Leu	Lys				
		225					230					235							
act	gta	ttc	cat	gct	cca	gat	ctg	agt	agg	atg	ctg	caa	atg	ttt	aga		922		
Thr	Val	Phe	His	Ala	Pro	Asp	Leu	Ser	Arg	Met	Leu	Gln	Met	Phe	Arg				
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gaa	ctg	aca	gct	gtc	cgg	tgc	tac	tgg	gtg	gat	gtc	aca	ctg	aat	tca		970		
Glu	Leu	Thr	Ala	Val	Arg	Cys	Tyr	Trp	Val	Asp	Val	Thr	Leu	Asn	Ser				
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gtc	aac	cta	aat	ttg	aat	ctt	gtc	ctt	tca	gaa	gat	cag	aga	caa	gtg		1018		
Val	Asn	Leu	Asn	Leu	Asn	Leu	Val	Leu	Ser	Glu	Asp	Gln	Arg	Gln	Val				
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Ile	Ser	Val	Pro	Ile	Trp	Pro	Phe	Gln	Cys	Tyr	Asn	Tyr	Gly	Val	Leu				
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gga	tcc	caa	tat	ttc	tcc	tct	ggg	aaa	cat	tac	tgg	gaa	gtg	gac	gtg		1114		
Gly	Ser	Gln	Tyr	Phe	Ser	Ser	Gly	Lys	His	Tyr	Trp	Glu	Val	Asp	Val				
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Ser	Lys	Lys	Thr	Ala	Trp	Ile	Leu	Gly	Val	Tyr	Cys	Arg	Thr	Tyr	Ser				
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cgc	cat	atg	aag	tat	gtt	gtt	aga	aga	tgt	gca	aat	cgt	caa	aat	ctt		1210		
Arg	His	Met	Lys	Tyr	Val	Val	Arg	Arg	Cys	Ala	Asn	Arg	Gln	Asn	Leu				
335					340					345					350				
tac	acc	aaa	tac	aga	cct	cta	ttt	ggc	tac	tgg	gtt	ata	ggg	tta	cag		1258		
Tyr	Thr	Lys	Tyr	Arg	Pro	Leu	Phe	Gly	Tyr	Trp	Val	Ile	Gly	Leu	Gln				
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293

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 Met Arg Thr Leu Phe Asn Leu Leu Trp Leu
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 Ala Leu Ala Cys Ser Pro Val His Thr Thr Leu Ser Lys Ser Asp Ala
 -5 1 5
 aaa aaa gcc gcc tca aag acg ctg ctg gag aag agt cag ttt tca gat 208
 Lys Lys Ala Ala Ser Lys Thr Leu Leu Glu Lys Ser Gln Phe Ser Asp
 10 15 20
 aag ccg gtg caa gac cgg ggt ttg gtg gtg acg gac ctc aaa gct gag 256
 Lys Pro Val Gln Asp Arg Gly Leu Val Val Thr Asp Leu Lys Ala Glu
 25 30 35
 agt gtg gtt ctt gag cat cgc agc tac tgc tgc gca aag gcc cgg gac 304
 Ser Val Val Leu Glu His Arg Ser Tyr Cys Ser Ala Lys Ala Arg Asp
 40 45 50 55
 aga cac ttt gct ggg gat gta ctg ggc tat gtc act cca tgg aac agc 352
 Arg His Phe Ala Gly Asp Val Leu Gly Tyr Val Thr Pro Trp Asn Ser
 60 65 70
 cat ggc tac gat gtc acc aag gtc ttt ggg agc aag ttc aca cag atc 400
 His Gly Tyr Asp Val Thr Lys Val Phe Gly Ser Lys Phe Thr Gln Ile
 75 80 85
 tca ccc gtc tgg ctg cag ttg aag aga cgt ggc cgt gag atg ttt gag 448
 Ser Pro Val Trp Leu Gln Leu Lys Arg Arg Gly Arg Glu Met Phe Glu
 90 95 100
 gtc acg ggc ctc cac gac gtg gac caa ggg tgg atg cga gct gtc agg 496
 Val Thr Gly Leu His Asp Val Asp Gln Gly Trp Met Arg Ala Val Arg
 105 110 115
 aag cat gcc aag ggc ctg cac ata gtg cct cgg ctc ctg ttt gag gac 544
 Lys His Ala Lys Gly Leu His Ile Val Pro Arg Leu Leu Phe Glu Asp
 120 125 130 135
 tgg act tac gat gat ttc cgg aac gtc tta gac agt gag gat gag ata 592
 Trp Thr Tyr Asp Asp Phe Arg Asn Val Leu Asp Ser Glu Asp Glu Ile
 140 145 150
 gag gag ctg agc aag acc gtg gtc cag gtg gca aag aac cag cat ttc 640
 Glu Glu Leu Ser Lys Thr Val Val Gln Val Ala Lys Asn Gln His Phe
 155 160 165
 gat ggc ttc gtg gtg gag gtc tgg aac cag ctg cta agc cag aag cgc 688
 Asp Gly Phe Val Val Glu Val Trp Asn Gln Leu Leu Ser Gln Lys Arg
 170 175 180

294

gtg ggc ctc atc cac atg ctc acc cac ttg gcc gag gcc ctg cac cag	736
Val Gly Leu Ile His Met Leu Thr His Leu Ala Glu Ala Leu His Gln	
185 190 195	
gcc cgg ctg ctg gcc ctc ctg gtc atc ccg cct gcc atc acc ccc ggg	784
Ala Arg Leu Leu Ala Leu Leu Val Ile Pro Pro Ala Ile Thr Pro Gly	
200 205 210 215	
acc gac cag ctg ggc atg ttc acg cac aag gag ttt gag cag ctg gcc	832
Thr Asp Gln Leu Gly Met Phe Thr His Lys Glu Phe Glu Gln Leu Ala	
220 225 230	
ccc gtg ctg gat ggt ttc agc ctc atg acc tac gac tac tct aca gcg	880
Pro Val Leu Asp Gly Phe Ser Leu Met Thr Tyr Asp Tyr Ser Thr Ala	
235 240 245	
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His Gln Pro Gly Pro Asn Ala Pro Leu Ser Trp Val Arg Ala Cys Val	
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cag gtc ctg gac ccg aag tcc aag tgg cga agc aaa atc ctc ctg ggg	976
Gln Val Leu Asp Pro Lys Ser Lys Trp Arg Ser Lys Ile Leu Leu Gly	
265 270 275	
ctc aac ttc tat ggt atg gac tac gcg acc tcc aag gat gcc cgt gag	1024
Leu Asn Phe Tyr Gly Met Asp Tyr Ala Thr Ser Lys Asp Ala Arg Glu	
280 285 290 295	
cct gtt gtc ggg gcc agg tac atc cag aca ctg aag gac cac agg ccc	1072
Pro Val Val Gly Ala Arg Tyr Ile Gln Thr Leu Lys Asp His Arg Pro	
300 305 310	
cgg atg gtg tgg gac agc cag gcc tca gag cac ttc ttc gag tac aag	1120
Arg Met Val Trp Asp Ser Gln Ala Ser Glu His Phe Phe Glu Tyr Lys	
315 320 325	
aag agc cgc agt ggg agg cac gtc gtc ttc tac cca acc ctg aag tcc	1168
Lys Ser Arg Ser Gly Arg His Val Val Phe Tyr Pro Thr Leu Lys Ser	
330 335 340	
ctg cag gtg cgg ctg gag ctg gcc cgg gag ctg ggc gtt ggg gtc tct	1216
Leu Gln Val Arg Leu Glu Leu Ala Arg Glu Leu Gly Val Gly Val Ser	
345 350 355	
atc tgg gag ctg ggc cag ggc ctg gac tac ttc tac gac ctg ctc	1261
Ile Trp Glu Leu Gly Gln Gly Leu Asp Tyr Phe Tyr Asp Leu Leu	
360 365 370	
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Met	

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Leu	Leu	Ser	Ile	Gly	Met	Leu	Met	Leu	Ser	Ala	Thr	Gln	Val	Tyr	Thr	
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gtc	ttg	act	gtc	cag	ctc	ttt	gca	ttc	tta	aac	cca	ctg	cct	gta	gaa	155
Val	Leu	Thr	Val	Gln	Leu	Phe	Ala	Phe	Leu	Asn	Pro	Leu	Pro	Val	Glu	
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gca	gac	att	tta	gca	tat	aac	ttt	gaa	aat	gca	tct	cag	aca	ttt	gat	203
Ala	Asp	Ile	Leu	Ala	Tyr	Asn	Phe	Glu	Asn	Ala	Ser	Gln	Thr	Phe	Asp	
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Asp	Leu	Pro	Ala	Arg	Phe	Gly	Tyr	Arg	Leu	Pro	Ala	Glu	Gly	Leu	Lys	
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Gly	Phe	Leu	Ile	Asn	Ser	Lys	Pro	Glu	Asn	Ala	Cys	Glu	Pro	Ile	Val	
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Pro	Pro	Pro	Val	Lys	Asp	Asn	Ser	Ser	Gly	Thr	Phe	Ile	Val	Leu	Ile	
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aga	aga	ctt	gat	tgt	aat	ttt	gat	ata	aag	gtt	tta	aat	gca	cag	aga	395
Arg	Arg	Leu	Asp	Cys	Asn	Phe	Asp	Ile	Lys	Val	Leu	Asn	Ala	Gln	Arg	
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Ala	Gly	Tyr	Lys	Ala	Ala	Ile	Val	His	Asn	Val	Asp	Ser	Asp	Asp	Leu	
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Ile	Ser	Met	Gly	Ser	Asn	Asp	Ile	Glu	Val	Leu	Lys	Lys	Ile	Asp	Ile	
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Pro	Ser	Val	Phe	Ile	Gly	Glu	Ser	Ser	Ala	Ser	Ser	Leu	Lys	Asp	Glu	
		135				140						145				
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Phe	Thr	Tyr	Glu	Lys	Gly	Gly	His	Leu	Ile	Leu	Val	Pro	Glu	Phe	Ser	
	150					155					160					
ctt	cct	ttg	gaa	tac	tac	cta	att	ccc	ttc	ctt	atc	ata	gtg	ggc	atc	635
Leu	Pro	Leu	Glu	Tyr	Tyr	Leu	Ile	Pro	Phe	Leu	Ile	Ile	Val	Gly	Ile	
165					170					175					180	
tgt	ctc	atc	ttg	ata	gtc	att	ttc	atg	atc	aca	aaa	ttt	gtc	cag	gat	683
Cys	Leu	Ile	Leu	Ile	Val	Ile	Phe	Met	Ile	Thr	Lys	Phe	Val	Gln	Asp	
				185				190						195		
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Arg	His	Arg	Ala	Arg	Arg	Asn	Arg	Leu	Arg	Lys	Asp	Gln	Leu	Lys	Lys	
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Leu	Pro	Val	His	Lys	Phe	Lys	Lys	Gly	Asp	Glu	Tyr	Asp	Val	Cys	Ala	
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Ile	Cys	Leu	Asp	Glu	Tyr	Glu	Asp	Gly	Asp	Lys	Leu	Arg	Ile	Leu	Pro	
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Cys	Ser	His	Ala	Tyr	His	Cys	Lys	Cys	Val	Asp	Pro	Trp	Leu	Thr	Lys	
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acc	aaa	aaa	acc	tgt	cca	gtg	tgc	agg	caa	aaa	gtt	gtt	cct	tct	caa	923
Thr	Lys	Lys	Thr	Cys	Pro	Val	Cys	Arg	Gln	Lys	Val	Val	Pro	Ser	Gln	
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ggc	gat	tca	gac	tct	gac	aca	gac	agt	agt	caa	gaa	gaa	aat	gaa	gtg	971
Gly	Asp	Ser	Asp	Ser	Asp	Thr	Asp	Ser	Ser	Gln	Glu	Glu	Asn	Glu	Val	
			280					285					290			
aca	gaa	cat	acc	cct	tta	ctg	aga	cct	tta	gct	tct	gtc	agt	gcc	cag	1019

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Ser	Phe	Gly	Ala	Leu	Ser	Glu	Ser	Arg	Ser	His	Gln	Asn	Met	Thr	Glu	
	310					315					320					
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Ser	Ser	Asp	Tyr	Glu	Glu	Asp	Asp	Asn	Glu	Asp	Thr	Asp	Ser	Ser	Asp	
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Ala	Glu	Asn	Glu	Ile	Asn	Glu	His	Asp	Val	Val	Val	Gln	Leu	Gln	Pro	
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aat	ggt	gaa	cgg	gat	tac	aac	ata	gca	aat	act	gtt	tgacttttcag				1209
Asn	Gly	Glu	Arg	Asp	Tyr	Asn	Ile	Ala	Asn	Thr	Val					
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<222> 72..197

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score 7.19999980926514

seq ILFSLSFLLVIIT/FP

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<222> 970..982

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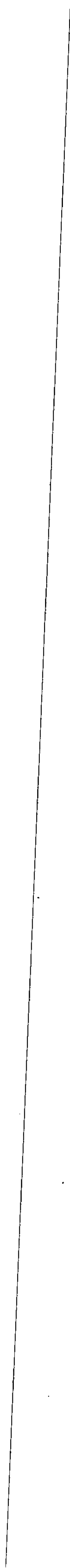
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Ser	Ile	Trp	Met	Cys	Leu	Lys	Ile
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Val	Phe	Arg	Leu	Gly	Arg	Ile	Gln
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Leu	Ile	Leu	Val	Leu	Pro	Cys	Ile
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Arg	Thr	Val	Thr	Cys	Asn	Ile	Pro
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Ser	Val	Thr	Thr	Gln	Val	Asp	Gly

297

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Ala	Val	Ser	Ala	Val	Ala	Asn	Val	Asn	Asp	Val	His	Gln	Ala	Thr	Phe	
85						90					95					
ctg	ctg	gct	caa	acc	act	ctg	aga	aat	gtc	tta	ggg	aca	cag	acc	ttg	542
Leu	Leu	Ala	Gln	Thr	Thr	Leu	Arg	Asn	Val	Leu	Gly	Thr	Gln	Thr	Leu	
100						105				110					115	
tcc	cag	atc	tta	gct	gga	cga	gaa	gag	atc	gcc	cat	agc	atc	cag	act	590
Ser	Gln	Ile	Leu	Ala	Gly	Arg	Glu	Glu	Ile	Ala	His	Ser	Ile	Gln	Thr	
				120					125					130		
tta	ctt	gat	gat	gcc	acc	gaa	ctg	tgg	ggg	atc	cgg	gtg	gcc	cga	gtg	638
Leu	Leu	Asp	Asp	Ala	Thr	Glu	Leu	Trp	Gly	Ile	Arg	Val	Ala	Arg	Val	
				135				140					145			
gaa	atc	aaa	gat	gtt	cgg	att	ccc	gtg	cag	ttg	cag	aga	tcc	atg	gca	686
Glu	Ile	Lys	Asp	Val	Arg	Ile	Pro	Val	Gln	Leu	Gln	Arg	Ser	Met	Ala	
		150				155						160				
gcc	gag	gct	gag	gcc	acc	cgg	gaa	gcg	aga	gcc	aag	gtc	ctt	gca	gct	734
Ala	Glu	Ala	Glu	Ala	Thr	Arg	Glu	Ala	Arg	Ala	Lys	Val	Leu	Ala	Ala	
		165				170						175				
gaa	gga	gaa	atg	agt	gct	tcc	aaa	tcc	ctg	aag	tca	gcc	tcc	atg	gtg	782
Glu	Gly	Glu	Met	Ser	Ala	Ser	Lys	Ser	Leu	Lys	Ser	Ala	Ser	Met	Val	
180					185				190						195	
ctg	gct	gag	tct	ccc	ata	gct	ctc	cag	ctg	cgc	tac	ctg	cag	acc	ttg	830
Leu	Ala	Glu	Ser	Pro	Ile	Ala	Leu	Gln	Leu	Arg	Tyr	Leu	Gln	Thr	Leu	
				200					205					210		
agc	acg	gta	gcc	acc	gag	aag	aat	tct	acg	att	gtg	ttt	cct	ctg	ccc	878
Ser	Thr	Val	Ala	Thr	Glu	Lys	Asn	Ser	Thr	Ile	Val	Phe	Pro	Leu	Pro	
			215					220				225				
atg	aat	ata	cta	gag	ggc	att	ggg	ggc	gtc	agc	tat	gat	aac	cac	aag	926
Met	Asn	Ile	Leu	Glu	Gly	Ile	Gly	Gly	Val	Ser	Tyr	Asp	Asn	His	Lys	
		230				235						240				
aag	ctt	cca	aat	aaa	gcc	tgaggtcctc	ttgcggtagt	cagctaaaaa	aaaaaaaa							982
Lys	Leu	Pro	Asn	Lys	Ala											
		245														

<210> 155
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 <213> Homo sapiens
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 <222> 425..430
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 <221> polyA_site
 <222> 443..455
 <400> 155

ggt	atg	cca	ccc	aga	aac	cta	ctg	gag	tta	ctt	att	aac	atc	aag	gct	48
Met	Pro	Pro	Arg	Asn	Leu	Leu	Glu	Leu	Leu	Ile	Asn	Ile	Lys	Ala		
1				5					10					15		
gga	acc	tat	ttg	cct	cag	tcc	tat	ctg	att	cat	gag	cac	atg	ggt	att	96
Gly	Thr	Tyr	Leu	Pro	Gln	Ser	Tyr	Leu	Ile	His	Glu	His	Met	Val	Ile	
				20				25						30		
act	gat	cgc	atc	gaa	aac	att	gat	cac	ctg	ggg	ttc	ttt	att	tat	cga	144
Thr	Asp	Arg	Ile	Glu	Asn	Ile	Asp	His	Leu	Gly	Phe	Phe	Ile	Tyr	Arg	
				35				40					45			
ctg	tgt	cat	gac	aag	gaa	act	tac	aaa	ctg	caa	cgc	aga	gaa	act	att	192
Leu	Cys	His	Asp	Lys	Glu	Thr	Tyr	Lys	Leu	Gln	Arg	Arg	Glu	Thr	Ile	
		50				55						60				



aaa ggt att cag aaa cgt gaa gcc agc aat tgt ttc gca att cgg cat	240
Lys Gly Ile Gln Lys Arg Glu Ala Ser Asn Cys Phe Ala Ile Arg His	
65 70 75	
ttt gaa aac aaa ttt gcc gtg gaa act tta att tgt tct tgaacagtca	289
Phe Glu Asn Lys Phe Ala Val Glu Thr Leu Ile Cys Ser	
80 85 90	
agaaaaacat tattgaggaa aattaatatc acagcataac cccacccttt acattttgtg	349
cagtgattat tttttaaaagt cttctttcat gtaagtagca aacagggctt tactatcttt	409
tcattctcatt aattcaatta aaaccattac cccaaaaaaa aaaaaa	455

<210> 156
 <211> 738
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 <213> Homo sapiens
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 <222> 90..278
 <223> Von Heijne matrix
 score 3.5
 seq GLVCAGLADMARF/AE
 <220>
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 <222> 704..709
 <220>
 <221> polyA_site
 <222> 724..738
 <400> 156

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accggtgtgc caacgatccc tcggcggtcg atg tcg gcc gcc ggt gcc cga ggc	113
Met Ser Ala Ala Gly Ala Arg Gly	
-60	
ctg cgg gcc acc tac cac cgg ctc ccc gat aaa gtg gag ctg atg ctg	161
Leu Arg Ala Thr Tyr His Arg Leu Pro Asp Lys Val Glu Leu Met Leu	
-55 -50 -45 -40	
ccc gag aaa ttg agg ccg ttg tac aac cat cca gca ggt ccc aga aca	209
Pro Glu Lys Leu Arg Pro Leu Tyr Asn His Pro Ala Gly Pro Arg Thr	
-35 -30 -25	
gtt ttc ttc tgg gct cca att atg aaa tgg ggg ttg gtg tgt gct gga	257
Val Phe Phe Trp Ala Pro Ile Met Lys Trp Gly Leu Val Cys Ala Gly	
-20 -15 -10	
ttg gct gat atg gcc aga cct gca gaa aaa ctt agc aca gct caa tct	305
Leu Ala Asp Met Ala Arg Pro Ala Glu Lys Leu Ser Thr Ala Gln Ser	
-5 1 5	
gct gtt ttg atg gct aca ggg ttt att tgg tca aga tac tca ctt gta	353
Ala Val Leu Met Ala Thr Gly Phe Ile Trp Ser Arg Tyr Ser Leu Val	
10 15 20 25	
att att ccg aaa aat tgg agt ctg ttt gct gtt aat ttc ttt gtg ggg	401
Ile Ile Pro Lys Asn Trp Ser Leu Phe Ala Val Asn Phe Phe Val Gly	
30 35 40	
gca gca gga gcc tct cag ctt ttt cgt att tgg aga tat aac caa gaa	449
Ala Ala Gly Ala Ser Gln Leu Phe Arg Ile Trp Arg Tyr Asn Gln Glu	
45 50 55	
cta aaa gct aaa gca cac aaa taaaagagtt cctgatcacc tgaacaatct	500
Leu Lys Ala Lys Ala His Lys	
60	
agatgtggac aaaaccattg ggacctagtt tattatttgg ttattgataa agcaaagcta	560
actgtgtgtt tagaaggcac tgtaactggt agctagttct tgattcaata gaaaaatgca	620
gcaaactttt aataacagtc tctctacatg acttaaggaa cttatctatg gatattagta	680

299

acatttttctt accatttgtc cgtaataaac catacttgct cgtaaaaaaa aaaaaaaa 738

<210> 157
<211> 649
<212> DNA
<213> Homo sapiens
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<222> 88..147
<223> Von Heijne matrix
score 12.3999996185303
seq ALLLGALLGTAWA/RR
<220>
<221> polyA_signal
<222> 619..624
<220>
<221> polyA_site
<222> 637..649
<400> 157

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aggaggagcg accccattac gctaaag atg aaa ggc tgg ggt tgg ctg gcc ctg 114
Met Lys Gly Trp Gly Trp Leu Ala Leu
-20 -15
ctt ctg ggg gcc ctg ctg gga acc gcc tgg gct cgg agg agc cag gat 162
Leu Leu Gly Ala Leu Leu Gly Thr Ala Trp Ala Arg Arg Ser Gln Asp
-10 -5 1 5
ctc cac tgt gga gca tgc agg gct ctg gtg gat gaa cta gaa tgg gaa 210
Leu His Cys Gly Ala Cys Arg Ala Leu Val Asp Glu Leu Glu Trp Glu
10 15 20
att gcc cag gtg gac ccc aag aag acc att cag atg gga tcc ttc cgg 258
Ile Ala Gln Val Asp Pro Lys Lys Thr Ile Gln Met Gly Ser Phe Arg
25 30 35
atc aat cca gat ggc agc cag tca gtg gtg gag gta act gtt act gtt 306
Ile Asn Pro Asp Gly Ser Gln Ser Val Val Glu Val Thr Val Thr Val
40 45 50
ccc cca aac aaa gta gct cac tct ggc ttt gga tgaaattcga ctgcttaaaa 359
Pro Pro Asn Lys Val Ala His Ser Gly Phe Gly
55 60
aggaccttgg tctaatagaa atgaagaaaa cagactcaga aaaaagattt ggctctgtct 419
catttggaag aagctgcagg cttattcccc atgcacttgc ttcctggctg caaaccttaa 479
tactttgttt ctgctgtaga atttgtttagc aaacagggag tcctgatcag cacccttctc 539
cacatccaca tgactggttt ttaatgtagc actgtggtat acatgcaaac atccgttcaa 599
aatctgagtc ggagctaaaa ataaaaaatg aaaaaacaaa aaaaaaaaaa 649

<210> 158
<211> 714
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 33..92
<223> Von Heijne matrix
score 12.3999996185303
seq ALLLGALLGTAWA/RR
<220>
<221> polyA_site
<222> 703..714
<400> 158

300



2

3

4

agcagaggtg gagcgacccc attacgctaa ag	atg aaa ggc tgg ggt tgg ctg	53
	Met Lys Gly Trp Gly Trp Leu	
	-20 -15	
gcc ctg ctt ctg ggg gcc ctg ctg gga acc gcc tgg gct cgg agg agc	101	
Ala Leu Leu Leu Gly Ala Leu Leu Gly Thr Ala Trp Ala Arg Arg Ser		
	-10 -5 1	
cag gat ctc cac tgt gga gca tgc agg gct ctg gtg gat gaa cta gaa	149	
Gln Asp Leu His Cys Gly Ala Cys Arg Ala Leu Val Asp Glu Leu Glu		
	5 10 15	
tgg gaa att gcc cag gtg gac ccc aag aag acc att cag atg gga tct	197	
Trp Glu Ile Ala Gln Val Asp Pro Lys Lys Thr Ile Gln Met Gly Ser		
	20 25 30 35	
ttc cgg atc aat cca gat ggc agc cag tca gtg gtg gag gtg cct tat	245	
Phe Arg Ile Asn Pro Asp Gly Ser Gln Ser Val Val Glu Val Pro Tyr		
	40 45 50	
gcc cgc tca gag gcc cac ctc aca gag ctg ctg gag gag ata tgt gac	293	
Ala Arg Ser Glu Ala His Leu Thr Glu Leu Leu Glu Glu Ile Cys Asp		
	55 60 65	
cgg atg aag gag tat ggg gaa cag att gat cct tcc acc cat cgc aag	341	
Arg Met Lys Glu Tyr Gly Glu Gln Ile Asp Pro Ser Thr His Arg Lys		
	70 75 80	
aac tac gta cgt gta gtg ggc cgg aat gga gaa tcc agt gaa ctg gac	389	
Asn Tyr Val Arg Val Val Gly Arg Asn Gly Glu Ser Ser Glu Leu Asp		
	85 90 95	
cta caa ggc atc cga atc gac tca gat att agc ggc acc ctc aag ttt	437	
Leu Gln Gly Ile Arg Ile Asp Ser Asp Ile Ser Gly Thr Leu Lys Phe		
	100 105 110 115	
gcg tgt ggg agc att gtg gag gaa tac gag gat gaa ctc att gaa ttc	485	
Ala Cys Gly Ser Ile Val Glu Glu Tyr Glu Asp Glu Leu Ile Glu Phe		
	120 125 130	
ttt tcc cga gag gct gac aat gtt aaa gac aaa ctt tgc agt aag cga	533	
Phe Ser Arg Glu Ala Asp Asn Val Lys Asp Lys Leu Cys Ser Lys Arg		
	135 140 145	
aca gat ctt tgt gac cat gcc ctg cac ata tcg cat gat gag cta	578	
Thr Asp Leu Cys Asp His Ala Leu His Ile Ser His Asp Glu Leu		
	150 155 160	
tgaaccactg gagcagccca cactggcttg atggatcacc cccaggaggg gaaaatggtg	638	
gcaatgcctt ttatatatta tgtttttact gaaattaact gaaaaaatat gaaacaaaa	698	
gtacaaaaaa aaaaaa	714	

<210> 159
 <211> 596
 <212> DNA
 <213> Homo sapiens
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 <221> sig_peptide
 <222> 33..107
 <223> Von Heijne matrix
 score 5
 seq MFAASLLAMCAGA/EV
 <220>
 <221> polyA_signal
 <222> 546..551
 <220>
 <221> polyA_site
 <222> 584..596
 <400> 159

cacagttcct ctcctcctag agcctgccga cc atg ccc gcg ggc gtg ccc atg	53
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	Met	Pro	Ala	Gly	Val	Pro	Met	
	-25					-20		
tcc acc tac ctg aaa atg ttc gca gcc agt ctc ctg gcc atg tgc gca								101
Ser Thr Tyr Leu Lys Met Phe Ala Ala Ser Leu Leu Ala Met Cys Ala								
	-15			-10		-5		
ggg gca gaa gtg gtg cac agg tac tac cga ccg gac ctg aca ata cct								149
Gly Ala Glu Val Val His Arg Tyr Tyr Arg Pro Asp Leu Thr Ile Pro								
	1			5		10		
gaa att cca cca aag cgt gga gaa ctc aaa acg gag ctt ttg gga ctg								197
Glu Ile Pro Pro Lys Arg Gly Glu Leu Lys Thr Glu Leu Leu Gly Leu								
	15		20		25		30	
aaa gaa aga aaa cac aaa cct caa gtt tct caa cag gag gaa ctt aaa								245
Lys Glu Arg Lys His Lys Pro Gln Val Ser Gln Gln Glu Glu Leu Lys								
	35		40		45			
taactatgcc aagaattctg tgaataatat aagtcttaaa tatgtatttc ttaatttatt								305
gcacaaact acttgctcctt aagcacttag tctaatagcta actgcaagag gaggtgctca								365
gtggatgttt agccgatacg ttgaaattta attacggttt gattgatatt tcttgaaaac								425
tgccaaagca catatcatca aaccatttca tgaatatggg ttggaagatg tttagtcttg								485
aatataacgc gaaatagaat atttgtaagt ctactatatg ggttgtcttt atttcatata								545
aattaagaaa ttatttaaaa ctatgaacta gtttcattaa aaaaaaaga a								596

<210> 160
 <211> 403
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> polyA_signal
 <222> 375..380
 <220>
 <221> polyA_site
 <222> 390..403
 <400> 160

tgaagagaat ggctgttgca gtcggcgctca gagcagctcc agtgccgggg attcggacgg	60
agagcgcgag gactcggcgg ctgagcgcg cgcacagcag ctagaggcgc tgctcaacaa	120
gact atg cgc att cgc atg aca gat gga cgg aca ctg gtc ggc tgc ttt	169
Met Arg Ile Arg Met Thr Asp Gly Arg Thr Leu Val Gly Cys Phe	
1 5 10 15	
ctc tgc act gac cgt gac tgc aat gtc atc ctg ggc tcg gcg cag gag	217
Leu Cys Thr Asp Arg Asp Cys Asn Val Ile Leu Gly Ser Ala Gln Glu	
	20 25 30
ttc ctc aag ccg tcg gat tcc ttc tct gcc ggg gag ccc cgt gtg ctg	265
Phe Leu Lys Pro Ser Asp Ser Phe Ser Ala Gly Glu Pro Arg Val Leu	
	35 40 45
ggc ctg gcc atg gta ccc gga cac cac atc gtt tcc att gag gtg cag	313
Gly Leu Ala Met Val Pro Gly His His Ile Val Ser Ile Glu Val Gln	
	50 55 60
agg gag agt ctg acc ggg cct ccg tat ctc tgaccacgat ggcgcttacc	363
Arg Glu Ser Leu Thr Gly Pro Pro Tyr Leu	
	65 70
tttcagactt cattaaactt atgacccaaa aaaaaaaaaa	403

<210> 161
 <211> 727
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> sig_peptide
 <222> 126..575

302



21

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<223> Von Heijne matrix
      score 8.60000038146973
      seq LELLTSCSPASA/SQ
<220>
<221> polyA_signal
<222> 670..675
<220>
<221> polyA_site
<222> 721..727
<220>
<221> misc_feature
<222> 257,376..377
<223> n=a, g, c or t
<400> 161
ctcagaactg tgctgggaag gatggtaggg cgactggggc tcacctccgc accgttgtag      60
gacccggggt agggttttga gcccgtagga gctgccccac gcggcctcgt cctgccaacg      120
gtcggg atg gcg gag acg aag gac aca gcg cag atg ttg gtg acc ttc aag      170
      Met Ala Glu Thr Lys Asp Thr Ala Gln Met Leu Val Thr Phe Lys
      -150              -145              -140
gat gtg gct gtg acc ttt acc cgg gag gag tgg aga cag ctg gac ctg      218
Asp Val Ala Val Thr Phe Thr Arg Glu Glu Trp Arg Gln Leu Asp Leu
-135              -130              -125              -120
gcc cag agg acc ctg tac cga gag ggc atc ggg ttc ccn aaa cca gag      266
Ala Gln Arg Thr Leu Tyr Arg Glu Gly Ile Gly Phe Pro Lys Pro Glu
              -115              -110              -105
ttg gtc cac ctg cta gag cat ggg cag gag ctg tgg ata gtg aag aga      314
Leu Val His Leu Leu Glu His Gly Gln Glu Leu Trp Ile Val Lys Arg
              -100              -95              -90
ggc ctc tca cat gct acc tgt gca gag ttt cac tct tgt tgc cca ggc      362
Gly Leu Ser His Ala Thr Cys Ala Glu Phe His Ser Cys Cys Pro Gly
              -85              -80              -75
tgg agt gca gtg gnn cgc cat ctc agc tca ctg caa ctt ctg cct ccc      410
Trp Ser Ala Val Xaa Arg His Leu Ser Ser Leu Gln Leu Leu Pro Pro
              -70              -65              -60
gag ttc aag gga ttc tcc tgc ctc agc ctc ccg agt agc tgg gat tac      458
Glu Phe Lys Gly Phe Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr
              -55              -50              -45              -40
agg cgc cca cca cca tgc ccg gct ggt ttt ttt gta ttt tta gta gag      506
Arg Arg Pro Pro Pro Cys Pro Ala Gly Phe Phe Val Phe Leu Val Glu
              -35              -30              -25
acg ggg ctt cac cat gtt ggc cag gct ggt ctt gaa ctc ttg acc tca      554
Thr Gly Leu His His Val Gly Gln Ala Gly Leu Glu Leu Leu Thr Ser
              -20              -15              -10
tgt agt cca ccc gcc tct gcc tcc caa agt gct gcg att aca ggc gtg      602
Cys Ser Pro Pro Ala Ser Ala Ser Gln Ser Ala Ala Ile Thr Gly Val
              -5              1              5
agc cac cgt gcc cgg cag aga aaa act gct taagggtgaa aagagaaatt      652
Ser His Arg Ala Arg Gln Arg Lys Thr Ala
10              15
taagaaattg ctgacggaat aaaaacataa tagaactaca acaccgaagg aaatgaaaga      712
agcaaaaaaa aaaaa      727

<210> 162
<211> 944
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide

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303


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<222> 90..155
<223> Von Heijne matrix
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      seq IILGCLALFLLLQ/RK
<220>
<221> polyA_signal
<222> 913..918
<220>
<221> polyA_site
<222> 932..944
<400> 162
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tctgcttctg gaaggtgctg gacaaaaaac atg gaa cta att tcc cca aca gtg      113
                               Met Glu Leu Ile Ser Pro Thr Val
                               -20                               -15
att ata atc ctg ggt tgc ctt gct ctg ttc tta ctc ctt cag cgg aag      161
Ile Ile Ile Leu Gly Cys Leu Ala Leu Phe Leu Leu Leu Gln Arg Lys
                               -10                               -5                               1
aat ttg cgt aga ccc ccg tgc atc aag ggc tgg att cct tgg att gga      209
Asn Leu Arg Arg Pro Pro Cys Ile Lys Gly Trp Ile Pro Trp Ile Gly
                               5                               10                               15
gtt gga ttt gag ttt ggg aaa gcc cct cta gaa ttt ata gag aaa gca      257
Val Gly Phe Glu Phe Gly Lys Ala Pro Leu Glu Phe Ile Glu Lys Ala
                               20                               25                               30
aga atc aag gta tgt ggt cgt ggc aga cgg ggt ctc cag agg aga caa      305
Arg Ile Lys Val Cys Gly Arg Gly Arg Arg Gly Leu Gln Arg Arg Gln
35                               40                               45                               50
tgc ttt ctt ttt taaactttct ttcattgact cttaagtga gggctagaac      357
Cys Phe Leu Phe
acggggaaca tacctgcttg cctcaactaa aggatctagt catttctgaa ttcctctact      417
aacaattaac aacaatatcc tgtgcaaaat tttgcgaaag aaatgaaata caattgcagc      477
gtgcatcgac atttttggaa gtagagatta acttttcgta tttttacttc atcgaagtta      537
agttccaaat gtgtatgtgt taagtaaagt ttttcagtaa ttgggaaaga taaagtgtaa      597
tccaatttaa gtttgtgaaa atgagtaatt cgtatccaaa ttggagttaa caccaaagta      657
ttgtacaaat tgcttgcaca gttggtccgt acacaataga caggctctgt attttttagct      717
gacgttggtta tttgatgatg atgtactcca ttttcactac ggcccgaaga gactagtaat      777
cctccttgta gtagatgttt ttgtcttgaa agtatctttt aaatgtctga gcactttaag      837
gaacagaccc ttattaatgt cttttaagtt ttattcaatt tccagtcaca aatattttat      897
ggatatttgat tgtctaataa atttgtatga tattaaaaaa aaaaaaa      944

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<210> 163
<211> 598
<212> DNA
<213> Homo sapiens
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<221> sig_peptide
<222> 126..287
<223> Von Heijne matrix
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      seq LETCGLLVSLVES/IW
<220>
<221> polyA_signal
<222> 561..566
<220>
<221> polyA_site
<222> 587..598
<400> 163
ctcagaactg tgctgggaag gatggtaggg cgactggggc tcacctccgc accgttgtag      60

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304

gacccgggggt aggggttttga gcccgtggga gctgccccac gcggcctcgt cctgccaacg	120
gtcgg atg gcg gag acg aag gac gca gcg cag atg ttg gtg acc ttc aag	170
Met Ala Glu Thr Lys Asp Ala Ala Gln Met Leu Val Thr Phe Lys	
-50 -45 -40	
gat gtg gct gtg acc ttt acc cgg gag gag tgg aga cag ctg gac ctg	218
Asp Val Ala Val Thr Phe Thr Arg Glu Glu Trp Arg Gln Leu Asp Leu	
-35 -30 -25	
gcc cag agg acc ctg tac cga gag gtg atg ctg gag acc tgt ggg ctt	266
Ala Gln Arg Thr Leu Tyr Arg Glu Val Met Leu Glu Thr Cys Gly Leu	
-20 -15 -10	
ctg gtt tca cta gtg gaa agc att tgg ctg cat ata aca gaa aac cag	314
Leu Val Ser Leu Val Glu Ser Ile Trp Leu His Ile Thr Glu Asn Gln	
-5 1 5	
atc aaa ctg gct tca cct gga agg aaa ttc act aac tcg cct gat gag	362
Ile Lys Leu Ala Ser Pro Gly Arg Lys Phe Thr Asn Ser Pro Asp Glu	
10 15 20 25	
aag cct gag gtg tgg ttg gct cca ggc ctg ttc ggt gcc gca gcc cag	410
Lys Pro Glu Val Trp Leu Ala Pro Gly Leu Phe Gly Ala Ala Ala Gln	
30 35 40	
tgacgccatc aaggatgtct tggttctctg ttccttcttc ttggttcagg cttctgattg	470
tcctcaggct ggctcctcat agggatgctg ggtgctgcag ccttgactgg ggcagcaggc	530
ccccatgttc aatccatcct cccaccttgg aataaatgct ttcttttcac aatgagaaaa	590
aaaaaaaa	598

<210> 164
 <211> 360
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> sig_peptide
 <222> 85..150
 <223> Von Heijne matrix
 score 5.90000009536743
 seq IILGCLALFLLLQ/RK
 <220>
 <221> polyA_site
 <222> 349..360
 <400> 164

caggttccgt agccacagaa aagaagcaag ggacggcagg actgtttcac actttttctgc	60
ttctggaagg tgctggacaa aaac atg gaa cta att tcc cca aca gtg att	111
Met Glu Leu Ile Ser Pro Thr Val Ile	
-20 -15	
ata atc ctg ggt tgc ctt gct ctg ttc tta ctc ctt cag cgg aag aat	159
Ile Ile Leu Gly Cys Leu Ala Leu Phe Leu Leu Leu Gln Arg Lys Asn	
-10 -5 1	
ttg cgt aga ccc ccg tgc atc aag ggc tgg att cct tgg att gga gtt	207
Leu Arg Arg Pro Pro Cys Ile Lys Gly Trp Ile Pro Trp Ile Gly Val	
5 10 15	
gga ttt gag ttt ggg aaa gcc cct cta gaa ttt ata gag aaa gca aga	255
Gly Phe Glu Phe Gly Lys Ala Pro Leu Glu Phe Ile Glu Lys Ala Arg	
20 25 30 35	
atc aag tat gga cca ata ttt aca gtc ttt gct atg gga aac cga atg	303
Ile Lys Tyr Gly Pro Ile Phe Thr Val Phe Ala Met Gly Asn Arg Met	
40 45 50	
acc ttt gtt act gaa gaa gaa gga att aat gtg ttt cta aaa tcc	348
Thr Phe Val Thr Glu Glu Glu Gly Ile Asn Val Phe Leu Lys Ser	
55 60 65	
aaaaaaaaaa aa	360


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<210> 165
<211> 490
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 77..124
<223> Von Heijne matrix
      score 4.80000019073486
      seq SLFIYIFLTCSNT/SP
<220>
<221> polyA_signal
<222> 461..466
<220>
<221> polyA_site
<222> 477..490
<400> 165
atgagcttcc agccccaaga gtggaggctg ccacatccca acatagtatc tattgaaaag      60
gaagcagtgt gtatct atg att ata tct ctg ttc atc tat ata ttt ttg aca      112
          Met Ile Ile Ser Leu Phe Ile Tyr Ile Phe Leu Thr
                    -15                    -10                    -5

tgt agc aac acc tct cca tct tat caa gga act caa ctc ggt ctg ggt      160
Cys Ser Asn Thr Ser Pro Ser Tyr Gln Gly Thr Gln Leu Gly Leu Gly
          1                    5                    10

ctc ccc agt gcc cag tgg tgg cct ttg aca ggt agg agg atg cag tgc      208
Leu Pro Ser Ala Gln Trp Trp Pro Leu Thr Gly Arg Arg Met Gln Cys
          15                    20                    25

tgc agg cta ttt tgt ttt ttg tta caa aac tgt ctt ttc cct ttt ccc      256
Cys Arg Leu Phe Cys Phe Leu Leu Gln Asn Cys Leu Phe Pro Phe Pro
          30                    35                    40

ctc cac ctg att cag cat gat ccc tgt gag ctg gtt ctc aca atc tcc      304
Leu His Leu Ile Gln His Asp Pro Cys Glu Leu Val Leu Thr Ile Ser
          45                    50                    55                    60

tgg gac tgg gct gag gca ggg gct tcg ctc tat tct ccc taaccatact      353
Trp Asp Trp Ala Glu Ala Gly Ala Ser Leu Tyr Ser Pro
          65                    70

gtcttccttt ccccttgcc acttagcagt tatcccccca gctatgcctt ctccctccct      413
cccttgccct ggcatatatt gtgccttatt tatgctgcaa atataacatt aaactatcaa      473
gtgaaaaaaaa aaaaaaa      490

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<210> 166
<211> 488
<212> DNA
<213> Homo sapiens
<220>
<221> polyA_signal
<222> 458..463
<220>
<221> polyA_site
<222> 475..488
<400> 166
ccgcttccga aaagagacag acaatgcagc catcata atg aag gtg gac aaa gac      55
          Met Lys Val Asp Lys Asp
                    1                    5

cgg cag atg gtg gtg ctg gag gaa gaa ttt cgg aac att tcc cca gag      103
Arg Gln Met Val Val Leu Glu Glu Glu Phe Arg Asn Ile Ser Pro Glu
          10                    15                    20

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306

gag ctc aaa atg gag ttg ccg gag aga cag ccc agg ttc gtg gtt tac	151
Glu Leu Lys Met Glu Leu Pro Glu Arg Gln Pro Arg Phe Val Val Tyr	
25 30 35	
agc tac aag tac gtg cgt gac gat ggc cga gtg tcc tac cct ttg tgt	199
Ser Tyr Lys Tyr Val Arg Asp Asp Gly Arg Val Ser Tyr Pro Leu Cys	
40 45 50	
ttc atc ttc tcc agc cct gtg ggc tgc aag ccg gaa caa cag atg atg	247
Phe Ile Phe Ser Ser Pro Val Gly Cys Lys Pro Glu Gln Gln Met Met	
55 60 65 70	
tat gca ggg agt aaa aac agg ctg gtg cag aca gca gag ctc aca aag	295
Tyr Ala Gly Ser Lys Asn Arg Leu Val Gln Thr Ala Glu Leu Thr Lys	
75 80 85	
gtg ttc gaa atc cgc acc act gat gac ctc act gag gcc tgg ctc caa	343
Val Phe Glu Ile Arg Thr Thr Asp Asp Leu Thr Glu Ala Trp Leu Gln	
90 95 100	
gaa aag ttg tct ttc ttt cgt tgatctctgg gctggggact gaattcctga	394
Glu Lys Leu Ser Phe Phe Arg	
105	
tgtctgagtc ctcaagggtga ctgggggactt ggaaccacctta ggacctgaac aaccaagact	454
ttaaataaat tttaaaatgc aaaaaaaaaa aaaa	488

<210> 167
 <211> 771
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> sig_peptide
 <222> 48..356
 <223> Von Heijne matrix
 score 4.90000009536743
 seq VYAFLGLTAPSGS/KE
 <220>
 <221> polyA_signal
 <222> 742..747
 <220>
 <221> polyA_site
 <222> 760..771
 <400> 167

ccacagccct tttcaggacc caaacaaccg cagccgctgt tcccagg atg gtg atc	56
Met Val Ile	
cgt gta tat att gca tct tcc tct ggc tct aca gcg att aag aag aaa	104
Arg Val Tyr Ile Ala Ser Ser Ser Gly Ser Thr Ala Ile Lys Lys Lys	
-100 -95 -90 -85	
caa caa gat gtg ctt ggt ttc cta gaa gcc aac aaa ata gga ttt gaa	152
Gln Gln Asp Val Leu Gly Phe Leu Glu Ala Asn Lys Ile Gly Phe Glu	
-80 -75 -70	
gaa aaa gat att gca gcc aat gaa gag aat cgg aag tgg atg aga gaa	200
Glu Lys Asp Ile Ala Ala Asn Glu Glu Asn Arg Lys Trp Met Arg Glu	
-65 -60 -55	
aat gta cct gag aat agt cga cca gcc aca ggt aac ccc ctg cca cct	248
Asn Val Pro Glu Asn Ser Arg Pro Ala Thr Gly Asn Pro Leu Pro Pro	
-50 -45 -40	
cag att ttc aat gaa agc cag tat cgc ggg gac tat gat gcc ttc ttt	296
Gln Ile Phe Asn Glu Ser Gln Tyr Arg Gly Asp Tyr Asp Ala Phe Phe	
-35 -30 -25	
gaa gcc aga gaa aat aat gca gtg tat gcc ttc tta ggc ttg aca gcc	344
Glu Ala Arg Glu Asn Asn Ala Val Tyr Ala Phe Leu Gly Leu Thr Ala	
-20 -15 -10 -5	


307

cca tct ggt tca aag gaa gca gaa gtg caa gca aag cag caa gca	389
Pro Ser Gly Ser Lys Glu Ala Glu Val Gln Ala Lys Gln Gln Ala	
1 5 10	
tgaaccttga gcactgtgct ttaagcatcc tgaaaaatga gtctccattg cttttataaa	449
atagcagaat tagctttgct tcaaaagaaa taggcttaat gttgaaataa tagattagtt	509
gggttttcac atgcaaacac tcaaaatgaa tacaaaatta aaatttgaac attatgggtga	569
ttatgggtgag gagaatggga tattaacata aaattatatt aataagtaga tatcgtagaa	629
atagtgttgt tacctgccaa gccatcctgt atacaccaat gattttacaa agaaaacacc	689
cttcctcct tctgccatta ctatggcaac ctaagtgtat ctgcagctct acattaaaaa	749
ggagaaagag aaaaaaaaaa aa	771

<210> 168
 <211> 959
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> sig_peptide
 <222> 69..359
 <223> Von Heijne matrix
 score 4
 seq RLPLVVSFIASSS/AN

<220>
 <221> polyA_signal
 <222> 927..932
 <220>
 <221> polyA_site
 <222> 947..959
 <400> 168

cggagagaac caggcagccc agaaacccca ggcgtggaga ttgatcctgc gagagaaggg	60
ggttcatc atg gcg gat gac cta aag cga ttc ttg tat aaa aag tta cca	110
Met Ala Asp Asp Leu Lys Arg Phe Leu Tyr Lys Lys Leu Pro	
-95 -90 -85	
agt gtt gaa ggg ctc cat gcc att gtt gtg tca gat aga gat gga gta	158
Ser Val Glu Gly Leu His Ala Ile Val Val Ser Asp Arg Asp Gly Val	
-80 -75 -70	
cct gtt att aaa gtg gca aat gac aat gct cca gag cat gct ttg cga	206
Pro Val Ile Lys Val Ala Asn Asp Asn Ala Pro Glu His Ala Leu Arg	
-65 -60 -55	
cct ggt ttc tta tcc act ttt gcc ctt gca aca gac caa gga agc aaa	254
Pro Gly Phe Leu Ser Thr Phe Ala Leu Ala Thr Asp Gln Gly Ser Lys	
-50 -45 -40	
ctt gga ctt tcc aaa aat aaa agt atc atc tgt tac tat aac acc tac	302
Leu Gly Leu Ser Lys Asn Lys Ser Ile Ile Cys Tyr Tyr Asn Thr Tyr	
-35 -30 -25 -20	
cag gtg gtt caa ttt aat cgt tta cct ttg gtg gtg agt ttc ata gcc	350
Gln Val Val Gln Phe Asn Arg Leu Pro Leu Val Val Ser Phe Ile Ala	
-15 -10 -5	
agc agc agt gcc aat aca gga cta att gtc agc cta gaa aag gaa ctt	398
Ser Ser Ser Ala Asn Thr Gly Leu Ile Val Ser Leu Glu Lys Glu Leu	
1 5 10	
gct cca ttg ttt gaa gaa ctg aga caa gtt gtg gaa gtt tct	440
Ala Pro Leu Phe Glu Glu Leu Arg Gln Val Val Glu Val Ser	
15 20 25	
taatctgaca gtggtttcag tgtgtacctt atcttcatta taacaacaca atatcaatcc	500
agcaatcttt agactacaat aatactttta tccatgtgct caagaaaggg cccctttttc	560
caacttatac taaagagcta gcatatagat gtaatttata gatagatcag ttgctatatt	620
ttctgggtgta gggctctttct tattttagtga gatctaggga taccacagaa atggttcagt	680
ctatcacagc tcccatggag ttagtctggg caccagatat ggatgagaga ttctattcag	740



tgatcagaa tcaaactggg acattgatcc acttgagccg ttaagtgtg ccaattgtac	800
aatatgccca ggcttgcaga ataaagccaa ctttttattg tgaataataa taaggacata	860
tttttcttca gattatgttt tattttctttg cattgagtga ggaacataaa atggcttggt	920
aaaagtaata aaatcagtac aatcactaaa aaaaaaaaaa	959

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<210> 169
<211> 464
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 33..98
<223> Von Heijne matrix
      score 9.80000019073486
      seq LVVFCLALQLVPG/SP
<220>
<221> polyA_signal
<222> 437..442
<220>
<221> polyA_site
<222> 455..464
<400> 169

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gccagaactt actcaccat cccactgaca cc atg aag cct gtg ctg cct ctc	53
Met Lys Pro Val Leu Pro Leu	
-20	
cag ttc ctg gtg gtg ttc tgc cta gca ctg cag ctg gtg cct ggg agt	101
Gln Phe Leu Val Val Phe Cys Leu Ala Leu Gln Leu Val Pro Gly Ser	
-15 -10 -5 1	
ccc aag cag cgt gtt ctg aag tat atc ttg gaa cct cca ccc tgc ata	149
Pro Lys Gln Arg Val Leu Lys Tyr Ile Leu Glu Pro Pro Pro Cys Ile	
5 10 15	
tca gca cct gaa aac tgt act cac ctg tgt aca atg cag gaa gat tgc	197
Ser Ala Pro Glu Asn Cys Thr His Leu Cys Thr Met Gln Glu Asp Cys	
20 25 30	
gag aaa gga ttt cag tgc tgt tcc tcc ttc tgt ggg ata gtc tgt tca	245
Glu Lys Gly Phe Gln Cys Cys Ser Ser Phe Cys Gly Ile Val Cys Ser	
35 40 45	
tca gaa aca ttt caa aag cgc aac aga atc aaa cac aag ggc tca gaa	293
Ser Glu Thr Phe Gln Lys Arg Asn Arg Ile Lys His Lys Gly Ser Glu	
50 55 60 65	
gtc atc atg cct gcc aac tgaggcatat ttcctagatc attttgcctc	341
Val Ile Met Pro Ala Asn	
70	
tacgatgttt tttcttggtc cacctttagg aaggtattga gaagcaagaa actggaggcc	401
caatatctaa cctgcaaatac gtttttgagt ttggcaataa aggctaatac accaaaaaaaa	461
aaa	464

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<210> 170
<211> 799
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 110..235
<223> Von Heijne matrix
      score 5.19999980926514
      seq LLFDLVCHEFCQS/DD
<220>

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<221> polyA_signal

<222> 764..769

<220>

<221> polyA_site

<222> 787..799

<400> 170

ccaaccccag gaagagtctg aagagcagcc agtgtttcgg cttgtgccct gtataacttga 60
agctgccaaa caagtacgtt ctgaaaatcc agaatggctt gatgtttac atg cac att 118
Met His Ile

-40

tta caa ctg ctt act aca gtg gat gat gga att caa gca att gta cat 166
Leu Gln Leu Leu Thr Thr Val Asp Asp Gly Ile Gln Ala Ile Val His

-35

-30

-25

tgt cct gac act gga aaa gac att tgg aat cta ctt ttt gac ctg gtc 214
Cys Pro Asp Thr Gly Lys Asp Ile Trp Asn Leu Leu Phe Asp Leu Val

-20

-15

-10

tgc cat gaa ttc tgc cag tct gat gat cca ccc atc att ctt caa gaa 262
Cys His Glu Phe Cys Gln Ser Asp Asp Pro Pro Ile Ile Leu Gln Glu

-5

1

5

cag aaa aca gtg cta gcc tct gtt ttt tca gtg ttg tct gcc atc tat 310
Gln Lys Thr Val Leu Ala Ser Val Phe Ser Val Leu Ser Ala Ile Tyr

10

15

20

25

gcc tca cag act gag caa gag tat cta aag ata gaa aaa gta gat ctt 358
Ala Ser Gln Thr Glu Gln Glu Tyr Leu Lys Ile Glu Lys Val Asp Leu

30

35

40

cct cta att gac agc ctc att cgg gtc tta caa aat atg gaa cag tgt 406
Pro Leu Ile Asp Ser Leu Ile Arg Val Leu Gln Asn Met Glu Gln Cys

45

50

55

cag aaa aaa cca gag aac tcg gca gag tct aac aca gag gaa act aaa 454
Gln Lys Lys Pro Glu Asn Ser Ala Glu Ser Asn Thr Glu Glu Thr Lys

60

65

70

agg act gat tta acc caa gat gat ttc cac ttg aaa atc tta aag gat 502
Arg Thr Asp Leu Thr Gln Asp Asp Phe His Leu Lys Ile Leu Lys Asp

75

80

85

att tta tgt gaa ttt ctt tct aat att ttt cag gca tta aca aag gag 550
Ile Leu Cys Glu Phe Leu Ser Asn Ile Phe Gln Ala Leu Thr Lys Glu

90

95

100

105

acg gtg gct cag gga gta aag gaa ggc cag ttg agc aaa cag aag tgt 598
Thr Val Ala Gln Gly Val Lys Glu Gly Gln Leu Ser Lys Gln Lys Cys

110

115

120

tcc tct gca ttt caa aac ctt ctt cct ttc tat agc cct gtg gtg gaa 646
Ser Ser Ala Phe Gln Asn Leu Leu Pro Phe Tyr Ser Pro Val Val Glu

125

130

135

gat ttt att aaa atc cta cgt gaa gtt gat aag gcg ctt gct gat gac 694
Asp Phe Ile Lys Ile Leu Arg Glu Val Asp Lys Ala Leu Ala Asp Asp

140

145

150

ttg gaa aaa aac ttc cca agt ttg aag gtt cag act taaaacctga 740
Leu Glu Lys Asn Phe Pro Ser Leu Lys Val Gln Thr

155

160

165

attggaatta cttctgtaca agaaataaac tttattttttc tcactgaaaa aaaaaaaaaa 799

<210> 171

<211> 320

<212> DNA

<213> Homo sapiens

<220>

<221> polyA_site

<222> 308..320

310


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<400> 171
tcattcatcca gagcagccag tgtccgggag gcagaag atg ccc cac tcc aag cct      55
                                Met Pro His Ser Lys Pro
                                1           5
ctg gac tgg ggg ctc tct tca gtg gct gaa tgt cca gca gag cta ttt      103
Leu Asp Trp Gly Leu Ser Ser Val Ala Glu Cys Pro Ala Glu Leu Phe
                10           15           20
cct tcc aca ggg ggc ctt gca ggg aag ggt cca gga ctt gac atc tta      151
Pro Ser Thr Gly Gly Leu Ala Gly Lys Gly Pro Gly Leu Asp Ile Leu
                25           30           35
aga tgc gtc ttg tcc cct tgg gcc agt cat ttc ccc tct ctg agc ctc      199
Arg Cys Val Leu Ser Pro Trp Ala Ser His Phe Pro Ser Leu Ser Leu
                40           45           50
ggg gtc ttc aac ctg tgaaatggga tcataatcac tgccttacct ccctcacggg      254
Gly Val Phe Asn Leu
55
tgttgtgagg actgagtgtg tggaagtttt tcataaactt tggatgctag tgtaaaaaaa      314
aaaaaa      320

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<210> 172
<211> 331
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 129..209
<223> Von Heijne matrix
        score 4.90000009536743
        seq CLLSYIALGAIHA/KI
<220>
<221> polyA_site
<222> 318..331
<400> 172

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atggaaacca gatgggggcaa cgggggtgggt ctagtgcaga ctgtagctgc agctcctctc      60
cacctctagc ctgctcattt ccagctcaga aattctacta atggcgtttt ttcttcctga      120
aaaaggaa atg aac agg gtc cct gct gat tct cca aat atg tgt cta atc      170
        Met Asn Arg Val Pro Ala Asp Ser Pro Asn Met Cys Leu Ile
                -25           -20           -15
tgt tta ctg agt tac ata gca ctt gga gcc atc cat gca aaa atc tgt      218
Cys Leu Leu Ser Tyr Ile Ala Leu Gly Ala Ile His Ala Lys Ile Cys
                -10           -5           1
agg aga gca ttc cag gaa gag gga aga gca aat gca aag acg ggc gtg      266
Arg Arg Ala Phe Gln Glu Glu Gly Arg Ala Asn Ala Lys Thr Gly Val
                5           10           15
aga gct tgg tgc ata cag cca tgg gcc aaa taaagtttcc ttggaatagc      316
Arg Ala Trp Cys Ile Gln Pro Trp Ala Lys
20           25
caaaaaaaaa aaaaa      331

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<210> 173
<211> 1075
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 78..359
<223> Von Heijne matrix
        score 4.19999980926514

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311


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seq IILTAVYFALSIS/LH
<220>
<221> polyA_signal
<222> 1042..1047
<220>
<221> polyA_site
<222> 1063..1075
<400> 173
gtggtaggga gcagccagga gcgggttttct gggaactgtg ggatgtgccc ttggggggccc      60
gagaaaacag aaggaag atg ctc cag acc agt aac tac agc ctg gtg ctc      110
          Met Leu Gln Thr Ser Asn Tyr Ser Leu Val Leu
                    -90                                -85
tct ctg cag ttc ctg ctg ctg tcc tat gac ctc ttt gtc aat tcc ttc      158
Ser Leu Gln Phe Leu Leu Leu Ser Tyr Asp Leu Phe Val Asn Ser Phe
          -80                                -75                                -70
tca gaa ctg ctc caa aag act cct gtc atc cag ctt gtg ctc ttc atc      206
Ser Glu Leu Leu Gln Lys Thr Pro Val Ile Gln Leu Val Leu Phe Ile
          -65                                -60                                -55
atc cag gat att gca gtc ctc ttc aac atc atc atc att ttc ctc atg      254
Ile Gln Asp Ile Ala Val Leu Phe Asn Ile Ile Ile Ile Phe Leu Met
          -50                                -45                                -40
ttc ttc aac acc ttc gtc ttc cag gct ggc ctg gtc aac ctc cta ttc      302
Phe Phe Asn Thr Phe Val Phe Gln Ala Gly Leu Val Asn Leu Leu Phe
          -35                                -30                                -25                                -20
cat aag ttc aaa ggg acc atc atc ctg aca gct gtg tac ttt gcc ctc      350
His Lys Phe Lys Gly Thr Ile Ile Leu Thr Ala Val Tyr Phe Ala Leu
          -15                                -10                                -5
agc atc tcc ctt cat gtc tgg gtc atg aac tta cgc tgg aaa aac tcc      398
Ser Ile Ser Leu His Val Trp Val Met Asn Leu Arg Trp Lys Asn Ser
          1                                5                                10
aac agc ttc ata tgg aca gat gga ctt caa atg ctg ttt gta ttc cag      446
Asn Ser Phe Ile Trp Thr Asp Gly Leu Gln Met Leu Phe Val Phe Gln
          15                                20                                25
aga cta gca gca gtg ttg tac tgc tac ttc tat aaa cgg aca gcc gta      494
Arg Leu Ala Ala Val Leu Tyr Cys Tyr Phe Tyr Lys Arg Thr Ala Val
          30                                35                                40                                45
aga cta ggc gat cct cac ttc tac cag gac tct ttg tgg ctg cgc aag      542
Arg Leu Gly Asp Pro His Phe Tyr Gln Asp Ser Leu Trp Leu Arg Lys
          50                                55                                60
gag ttc atg caa gtt cga agg tgacctcttg tcacactgat ggatactttt      593
Glu Phe Met Gln Val Arg Arg
          65
ccttcctgat agaagccaca tttgctgctt tgcagggaga gttggcccta tgcattgggca      653
aacagctgga ctttccaagg aagggttcaga ctagctgtgt tcagcattca agaaggaaga      713
tccccctct tgcacaatta gtagtgcctc atcggtctcc agtgccggcat cccttccttg      773
ccttctacct ctgttccacc cccttccttc ctctcctctc tgtaccattc attctccctg      833
accggccttt cttgccgagg gttctgtggc tcttaccctt gtgaagcttt tccttttagcc      893
tgggacagaa ggacctcccg gccccaaag gatctcccag tgaccaaaagg atgcgaagag      953
tgatagttac gtgctcctga ctgatcacac cgcagacatt tagattttta taccgaaggc      1013
actttaaaaa aatgttttat aaatagagaa taaattgaat tcttggtcca aaaaaaaaaa      1073
aa
          1075

<210> 174
<211> 632
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide

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312



15
16
17
18
19

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<222> 62..265
<223> Von Heijne matrix
      score 4.59999990463257
      seq LPFSLVSMMLVTQG/LV
<220>
<221> polyA_signal
<222> 602..607
<220>
<221> polyA_site
<222> 621..632
<400> 174
cactgggtca aggagtaagc agaggataaa caactggaag gagagcaagc acaaagtcac      60
c atg gct tca gcg tct gct cgt gga aac caa gat aaa gat gcc cat ttt      109
  Met Ala Ser Ala Ser Ala Arg Gly Asn Gln Asp Lys Asp Ala His Phe
      -65                      -60                      -55
cca cca cca agc aag cag agc ctg ttg ttt tgt cca aaa tca aaa ctg      157
Pro Pro Pro Ser Lys Gln Ser Leu Leu Phe Cys Pro Lys Ser Lys Leu
      -50                      -45                      -40
cac atc cac aga gca gag atc tca aag att atg cga gaa tgt cag gaa      205
His Ile His Arg Ala Glu Ile Ser Lys Ile Met Arg Glu Cys Gln Glu
      -35                      -30                      -25
gaa agt ttc tgg aag aga gct ctg cct ttt tct ctt gta agc atg ctt      253
Glu Ser Phe Trp Lys Arg Ala Leu Pro Phe Ser Leu Val Ser Met Leu
      -20                      -15                      -10                      -5
gtc acc cag gga cta gtc tac caa ggt tat ttg gca gct aat tct aga      301
Val Thr Gln Gly Leu Val Tyr Gln Gly Tyr Leu Ala Ala Asn Ser Arg
      1                      5                      10
ttt gga tca ttg ccc aaa gtt gca ctt gct ggt ctc ttg gga ttt ggc      349
Phe Gly Ser Leu Pro Lys Val Ala Leu Ala Gly Leu Leu Gly Phe Gly
      15                      20                      25
ctt gga aag gta tca tac ata gga gta tgc cag agt aaa ttc cat ttt      397
Leu Gly Lys Val Ser Tyr Ile Gly Val Cys Gln Ser Lys Phe His Phe
      30                      35                      40
ttt gaa gat cag ctc cgt ggg gct ggt ttt ggt cca cag cat aac agg      445
Phe Glu Asp Gln Leu Arg Gly Ala Gly Phe Gly Pro Gln His Asn Arg
      45                      50                      55                      60
cac tgc ctc ctt acc tgt gag gaa tgc aaa ata aag cat gga tta agt      493
His Cys Leu Leu Thr Cys Glu Glu Cys Lys Ile Lys His Gly Leu Ser
      65                      70                      75
gag aag gga gac tct cag cct tca gct tcc taaattctgt gtctgtgact      543
Glu Lys Gly Asp Ser Gln Pro Ser Ala Ser
      80                      85
ttcgaagttt tttaaacctc tgaatttgta cacattttaa atttcaagtg tacttttaaaa      603
taaaatactt ctaatgtaaa aaaaaaaaaa      632

<210> 175
<211> 430
<212> DNA
<213> Homo sapiens
<220>
<221> polyA_signal
<222> 402..407
<220>
<221> polyA_site
<222> 419..430
<400> 175
gtattgggaa agtgatttgt gaa atg aaa gta gaa gaa gag cat acc aat gca      53
      Met Lys Val Glu Glu Glu His Thr Asn Ala

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313



100



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seq SFLPSALVIWTS/AF
<220>
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<222> 550..555
<220>
<221> polyA_site
<222> 574..585
<400> 177
cacgttctctg ttgagtacac gttcctgttg atttacaaaa ggtgcaggta tgagcaggtc      60
tgaagactaa cattttgtga agttgtaaaa cagaaaacct gttagaa atg tgg tgg      116
                                   Met Trp Trp
                                   -20
ttt cag caa ggc ctc agt ttc ctt cct tca gcc ctt gta att tgg aca      164
Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val Ile Trp Thr
               -15               -10               -5
tct gct gct ttc ata ttt tca tac att act gca gta aca ctc cac cat      212
Ser Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr Leu His His
               1               5               10
ata gac ccg gct tta cct tat atc agt gac act ggt aca gta gct cca      260
Ile Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr Val Ala Pro
15               20               25               30
gaa aaa tgc tta ttt ggg gca atg cta aat att gcg gca gtc tta tgt      308
Glu Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala Val Leu Cys
               35               40               45
caa aaa tagaaatcag gaagataatt caacttaaag aagttcattt catgaccaa      364
Gln Lys
ctcttcagaa acatgtcttt acaagcatat ctcttgtatt gctttctaca ctgttgaatt      424
gtctggcaat atttctgcag tggaaaattt gatttagcta gttcttgact gataaatatg      484
gtaagggtggg cttttcccc tgtgtaattg gctactatgt cttactgagc caagttgtaa      544
tttgaaataa aatgatatga gagtgcacaca aaaaaaaaaa a      585

<210> 178
<211> 613
<212> DNA
<213> Homo sapiens
<220>
<221> sig_peptide
<222> 118..171
<223> Von Heijne matrix
      score 5.90000009536743
      seq ALALLWSLPASDL/GR
<220>
<221> polyA_signal
<222> 583..588
<220>
<221> polyA_site
<222> 602..613
<400> 178
ggggtgggtg gactagaagc atttgggagt agtggccagg ggccctggac gctagccacg      60
gagctgccgc acagagcctg gtgtccacaa gcttccagggt tgggggttga gcctggg      117
atg agc ccc ggc agc gcc ttg gcc ctt ctg tgg tcc ctg cca gcc tct      165
Met Ser Pro Gly Ser Ala Leu Ala Leu Leu Trp Ser Leu Pro Ala Ser
               -15               -10               -5
gac ctg ggc cgg tca gtc att gct gga ctc tgg cca cac act ggc gtt      213
Asp Leu Gly Arg Ser Val Ile Ala Gly Leu Trp Pro His Thr Gly Val
               1               5               10
ctc atc cac ttg gaa aca agc cag tct ttt ctg caa ggt cag ttg acc      261
Leu Ile His Leu Glu Thr Ser Gln Ser Phe Leu Gln Gly Gln Leu Thr

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315

15		20		25		30	
aag agc ata ttt ccc ctc tgt tgt aca tcg ttg ttt tgt gtt tgt gtt							309
Lys Ser Ile Phe Pro Leu Cys Cys Thr Ser Leu Phe Cys Val Cys Val							
	35		40		45		
gta aca gtg ggt gga ggg agg gtg ggg tct aca ttt gtt gca							351
Val Thr Val Gly Gly Gly Arg Val Gly Ser Thr Phe Val Ala							
	50		55		60		
tgagtcgatg ggtcagaact ttagtatacg catgcgtcct ctgagtgaca gggcattttg							411
tcgaaaataa gcaccttggg aactaaaccc ctctaatagc tataaaggct ttagttctgt							471
attgattaag ttactgtaaa agcttggggtt tattttttgta ggacttaatg gctaagaatt							531
agaacatagc aagggggctc ctctgttgga gtaatgtaaa ttgtaattat aaataaacat							591
gcaaaccctt aaaaaaaaaa aa							613

<210> 179
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 <221> sig_peptide
 <222> 128..268
 <223> Von Heijne matrix
 score 5.5
 seq SALLFFARPCVFC/FK

<220>	
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<222> 410..415	
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<221> polyA_site	
<222> 424..427	
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agcttgggatt tacactgggc aacgtgggttg gaatgtatct ggctcagaac tatgatatac	60
caaacctggc taataaaactt gaagaaatta aaaaggactt ggatgccaaag aagaaacccc	120
ctagtgc atg aga ctg cct cca gca ctg cct tca gga tat act gat tct	169
Met Arg Leu Pro Pro Ala Leu Pro Ser Gly Tyr Thr Asp Ser	
	-45 -40 -35
act gct ctt gag ggc ctc gtt tac tat ctg aac caa aag ctt ttg ttt	217
Thr Ala Leu Glu Gly Leu Val Tyr Tyr Leu Asn Gln Lys Leu Leu Phe	
	-30 -25 -20
tcg tct cca gcc tca gca ctt ctc ttc ttt gct aga ccc tgt gtt ttt	265
Ser Ser Pro Ala Ser Ala Leu Leu Phe Phe Ala Arg Pro Cys Val Phe	
	-15 -10 -5
tgc ttt aaa gca agc aaa atg ggg ccc caa ttt gag aac tac cca aca	313
Cys Phe Lys Ala Ser Lys Met Gly Pro Gln Phe Glu Asn Tyr Pro Thr	
1 5 10 15	
ttt cca aca tac tca cct ctt ccc ata atc cct ttc caa ctg cat ggg	361
Phe Pro Thr Tyr Ser Pro Leu Pro Ile Ile Pro Phe Gln Leu His Gly	
	20 25 30
agg ttc taagactgga attatgggtgc tagattagta aacatgactt ttaatgaaaa	417
Arg Phe	
aaaaacaaaa	427

<210> 180
 <211> 905
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> sig_peptide
 <222> 149..457

316

<223> Von Heijne matrix
 score 4.90000009536743
 seq FLLAQTTLRNVLG/TQ

<220>

<221> polyA_site

<222> 893..912

<400> 180

gctgcctggt cttcacactt agctccaaac ccatgaaaaa ttgccaagta taaaagcttc 60
 tcaagaatga gatggattct aggggtgtctt cacctgagaa gcaagataaa gagaatttcg 120
 tgggtgtcaa caataaacgg cttgggtgt atg tgg ctg gat cct gtt ttc cct 172
 Met Trp Leu Asp Pro Val Phe Pro

-100

ctc ttt cct gtt ggt gat cat tac ctt ccc cat ctc cat atg gat gtg 220
 Leu Phe Pro Val Gly Asp His Tyr Leu Pro His Leu His Met Asp Val
 -95 -90 -85 -80

ctt gaa ggt ttg atc ctg gtc ctg cca tgc ata gat gtg ttt gtc aaa 268
 Leu Glu Gly Leu Ile Leu Val Leu Pro Cys Ile Asp Val Phe Val Lys
 -75 -70 -65

gtt gac ctc cga aca gtt act tgc aac att cct cca caa gag atc ctc 316
 Val Asp Leu Arg Thr Val Thr Cys Asn Ile Pro Pro Gln Glu Ile Leu
 -60 -55 -50

acc aga gac tcc gta act act cag gta gat gga gtt gtc tat tac aga 364
 Thr Arg Asp Ser Val Thr Thr Gln Val Asp Gly Val Val Tyr Tyr Arg
 -45 -40 -35

atc tat agt gct gtc tca gca gtg gct aat gtc aac gat gtc cat caa 412
 Ile Tyr Ser Ala Val Ser Ala Val Ala Asn Val Asn Asp Val His Gln
 -30 -25 -20

gca aca ttt ctg ctg gct caa acc act ctg aga aat gtc tta ggg aca 460
 Ala Thr Phe Leu Leu Ala Gln Thr Thr Leu Arg Asn Val Leu Gly Thr
 -15 -10 -5 1

cag acc ttg tcc cag atc tta gct gga cga gaa gag atc gcc cat agc 508
 Gln Thr Leu Ser Gln Ile Leu Ala Gly Arg Glu Glu Ile Ala His Ser
 5 10 15

atc cag act tta ctt gat gat gcc acc gaa ctg tgg ggg atc cgg gtg 556
 Ile Gln Thr Leu Leu Asp Asp Ala Thr Glu Leu Trp Gly Ile Arg Val
 20 25 30

gcc cga gtg gaa atc aaa gat gtt cgg att ccc gtg cag ttg cag aga 604
 Ala Arg Val Glu Ile Lys Asp Val Arg Ile Pro Val Gln Leu Gln Arg
 35 40 45

tcc atg gca gcc gag gct gag gcc acc cgg gaa gcg aga gcc aag gtc 652
 Ser Met Ala Ala Glu Ala Glu Ala Thr Arg Glu Ala Arg Ala Lys Val
 50 55 60 65

ctt gca gct gaa gga gaa atg aat gct tcc aaa tcc ctg aag tca gcc 700
 Leu Ala Ala Glu Gly Glu Met Asn Ala Ser Lys Ser Leu Lys Ser Ala
 70 75 80

tcc atg gtg ctg gct gag tct ccc ata gct ctc cag ctg cgc tac ctg 748
 Ser Met Val Leu Ala Glu Ser Pro Ile Ala Leu Gln Leu Arg Tyr Leu
 85 90 95

cag acc ttg agc acg gta gcc acc gag aag aat tct acg att gtg ttt 796
 Gln Thr Leu Ser Thr Val Ala Thr Glu Lys Asn Ser Thr Ile Val Phe
 100 105 110

cct ctg ccc atg aat ata cta gag ggc att ggt ggc gtc agc tat gat 844
 Pro Leu Pro Met Asn Ile Leu Glu Gly Ile Gly Gly Val Ser Tyr Asp
 115 120 125

aac cac aag aag ctt cca aat aaa gcc tgagggtcctc ttgcggtagt 891
 Asn His Lys Lys Leu Pro Asn Lys Ala

130 135
 caaaaaaaaaaaaa 905

317



2000
2001
2002
2003

<210> 181
 <211> 307
 <212> PRT
 <213> Homo sapiens
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 <221> SIGNAL
 <222> -13...-1
 <400> 181

Met	Leu	Ala	Val	Ser	Leu	Thr	Val	Pro	Leu	Leu	Gly	Ala	Met	Met	Leu
			-10					-5					1		
Leu	Glu	Ser	Pro	Ile	Asp	Pro	Gln	Pro	Leu	Ser	Phe	Lys	Glu	Pro	Pro
5						10					15				
Leu	Leu	Leu	Gly	Val	Leu	His	Pro	Asn	Thr	Lys	Leu	Arg	Gln	Ala	Glu
20					25				30						35
Arg	Leu	Phe	Glu	Asn	Gln	Leu	Val	Gly	Pro	Glu	Ser	Ile	Ala	His	Ile
				40				45						50	
Gly	Asp	Val	Met	Phe	Thr	Gly	Thr	Ala	Asp	Gly	Arg	Val	Val	Lys	Leu
			55					60					65		
Glu	Asn	Gly	Glu	Ile	Glu	Thr	Ile	Ala	Arg	Phe	Gly	Ser	Gly	Pro	Cys
		70				75					80				
Lys	Thr	Arg	Gly	Asp	Glu	Pro	Val	Cys	Gly	Arg	Pro	Leu	Gly	Ile	Arg
	85					90					95				
Ala	Gly	Pro	Asn	Gly	Thr	Leu	Phe	Val	Ala	Asp	Ala	Tyr	Lys	Gly	Leu
100					105					110					115
Phe	Glu	Val	Asn	Pro	Trp	Lys	Arg	Glu	Val	Lys	Leu	Leu	Leu	Ser	Ser
				120					125					130	
Glu	Thr	Pro	Ile	Glu	Gly	Lys	Asn	Met	Ser	Phe	Val	Asn	Asp	Leu	Thr
			135					140					145		
Val	Thr	Gln	Asp	Gly	Arg	Lys	Ile	Tyr	Phe	Thr	Asp	Ser	Ser	Ser	Lys
		150					155					160			
Trp	Gln	Arg	Arg	Asp	Tyr	Leu	Leu	Leu	Val	Met	Glu	Gly	Thr	Asp	Asp
	165					170					175				
Gly	Arg	Leu	Leu	Glu	Tyr	Asp	Thr	Val	Thr	Arg	Glu	Val	Lys	Val	Leu
180					185					190					195
Leu	Asp	Gln	Leu	Arg	Phe	Pro	Asn	Gly	Val	Gln	Leu	Ser	Pro	Ala	Glu
				200					205					210	
Asp	Phe	Val	Leu	Val	Ala	Glu	Thr	Thr	Met	Ala	Arg	Ile	Arg	Arg	Val
			215					220					225		
Tyr	Val	Ser	Gly	Leu	Met	Lys	Gly	Gly	Ala	Asp	Leu	Phe	Val	Glu	Asn
		230				235						240			
Met	Pro	Gly	Phe	Pro	Asp	Asn	Ile	Arg	Pro	Ser	Ser	Ser	Gly	Gly	Tyr
	245					250					255				
Trp	Val	Gly	Met	Ser	Thr	Ile	Arg	Pro	Asn	Pro	Gly	Phe	Ser	Met	Leu
260					265					270					275
Asp	Phe	Leu	Ser	Glu	Arg	Pro	Trp	Ile	Lys	Arg	Met	Ile	Phe	Lys	Val
				280					285					290	

Lys Lys Lys

<210> 182
 <211> 59
 <212> PRT
 <213> Homo sapiens
 <400> 182

Met	Met	Tyr	Val	Ser	Ile	Glu	Met	Ser	Gly	Pro	Thr	Ile	Ser	His	Leu
1				5					10					15	
Phe	Asp	Tyr	Val	Val	Cys	Tyr	Ile	Tyr	Gly	Leu	Lys	Ser	Phe	Ser	Leu
			20					25					30		



Lys Gln Leu Lys Lys Lys Ser Trp Ser Lys Tyr Leu Phe Glu Ser Cys
 35 40 45
 Cys Tyr Arg Ser Leu Tyr Val Cys Val Phe Ile
 50 55

<210> 183
 <211> 97
 <212> PRT
 <213> Homo sapiens
 <220>

<221> SIGNAL
 <222> -28...-1
 <400> 183

Met Ser Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly
 -25 -20 -15
 Val Leu Leu Glu Pro Phe Val His Gln Val Gly Gly His Ser Cys Val
 -10 -5 1
 Leu Arg Phe Asn Glu Thr Thr Leu Cys Lys Pro Leu Val Pro Arg Glu
 5 10 15 20
 His Gln Phe Tyr Glu Thr Leu Pro Ala Glu Met Arg Lys Phe Ser Pro
 25 30 35
 Gln Tyr Lys Gly Gln Ser Gln Arg Pro Leu Val Ser Trp Pro Ser Leu
 40 45 50
 Pro His Phe Phe Pro Trp Ser Phe Pro Leu Trp Pro Gln Gly Ser Val
 55 60 65
 Ala

<210> 184
 <211> 52
 <212> PRT
 <213> Homo sapiens
 <220>

<221> SIGNAL
 <222> -32...-1
 <400> 184

Met Leu Gly Thr Thr Gly Leu Gly Thr Gln Gly Pro Ser Gln Gln Ala
 -30 -25 -20
 Leu Gly Phe Phe Ser Phe Met Leu Leu Gly Met Gly Gly Cys Leu Pro
 -15 -10 -5
 Gly Phe Leu Leu Gln Pro Pro Asn Arg Ser Pro Thr Leu Pro Ala Ser
 1 5 10 15
 Thr Phe Ala His
 20

<210> 185
 <211> 124
 <212> PRT
 <213> Homo sapiens
 <220>

<221> SIGNAL
 <222> -97...-1
 <400> 185

Met Ala Asp Asp Leu Lys Arg Phe Leu Tyr Lys Lys Leu Pro Ser Val
 -95 -90 -85
 Glu Gly Leu His Ala Ile Val Val Ser Asp Arg Asp Gly Val Pro Val
 -80 -75 -70
 Val Lys Val Ala Asn Asp Asn Ala Pro Glu His Ala Leu Arg Pro Gly
 -65 -60 -55 -50

319

Phe	Leu	Ser	Thr	Phe	Ala	Leu	Ala	Thr	Asp	Gln	Gly	Ser	Lys	Leu	Gly
				-45					-40					-35	
Leu	Ser	Lys	Asn	Lys	Ser	Ile	Ile	Cys	Tyr	Tyr	Asn	Thr	Tyr	Gln	Val
			-30					-25					-20		
Val	Gln	Phe	Asn	Arg	Leu	Pro	Leu	Val	Val	Ser	Phe	Ile	Ala	Ser	Ser
		-15					-10					-5			
Ser	Ala	Asn	Thr	Gly	Leu	Ile	Val	Ser	Leu	Glu	Lys	Glu	Leu	Ala	Pro
1					5				10						15
Leu	Phe	Glu	Glu	Leu	Arg	Gln	Val	Val	Glu	Val	Ser				
				20					25						

<210> 186
 <211> 230
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -24...-1
 <400> 186

Met	Ala	Ser	Leu	Gly	Leu	Gln	Leu	Val	Gly	Tyr	Ile	Leu	Gly	Leu	Leu
				-20					-15					-10	
Gly	Leu	Leu	Gly	Thr	Leu	Val	Ala	Met	Leu	Leu	Pro	Ser	Trp	Lys	Thr
			-5					1				5			
Ser	Ser	Tyr	Val	Gly	Ala	Ser	Ile	Val	Thr	Ala	Val	Gly	Phe	Ser	Lys
10					15					20					
Gly	Leu	Trp	Met	Glu	Cys	Ala	Thr	His	Ser	Thr	Gly	Ile	Thr	Gln	Cys
25				30					35					40	
Asp	Ile	Tyr	Ser	Thr	Leu	Leu	Gly	Leu	Pro	Ala	Asp	Ile	Gln	Ala	Ala
				45					50				55		
Gln	Ala	Met	Met	Val	Thr	Ser	Ser	Ala	Ile	Ser	Ser	Leu	Ala	Cys	Ile
			60					65				70			
Ile	Ser	Val	Val	Gly	Met	Arg	Cys	Thr	Val	Phe	Cys	Gln	Glu	Ser	Arg
		75				80					85				
Ala	Lys	Asp	Arg	Val	Ala	Val	Ala	Gly	Gly	Val	Phe	Phe	Ile	Leu	Gly
90					95					100					
Gly	Leu	Leu	Gly	Phe	Ile	Pro	Val	Ala	Trp	Asn	Leu	His	Gly	Ile	Leu
105				110					115					120	
Arg	Asp	Phe	Tyr	Ser	Pro	Leu	Val	Pro	Asp	Ser	Met	Lys	Phe	Glu	Ile
				125					130					135	
Gly	Glu	Ala	Leu	Tyr	Leu	Gly	Ile	Ile	Ser	Ser	Leu	Phe	Ser	Leu	Ile
			140				145					150			
Ala	Gly	Ile	Ile	Leu	Cys	Phe	Ser	Cys	Ser	Ser	Gln	Arg	Asn	Arg	Ser
		155				160					165				
Asn	Tyr	Tyr	Asp	Ala	Tyr	Gln	Ala	Gln	Pro	Leu	Ala	Thr	Arg	Ser	Ser
170					175				180						
Pro	Arg	Pro	Gly	Gln	Pro	Pro	Lys	Val	Lys	Ser	Glu	Phe	Asn	Ser	Tyr
185				190					195						200
Ser	Leu	Thr	Gly	Tyr	Val										
				205											

<210> 187
 <211> 72
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -32...-1
 <400> 187

320

Met	Phe	Ala	Leu	Ala	Val	Met	Arg	Ala	Phe	Arg	Lys	Asn	Lys	Thr	Leu
		-30					-25					-20			
Gly	Tyr	Gly	Val	Pro	Met	Leu	Leu	Leu	Ile	Ala	Gly	Gly	Ser	Phe	Gly
	-15					-10				-5					
Leu	Arg	Glu	Phe	Ser	Gln	Ile	Arg	Tyr	Asp	Ala	Val	Lys	Ser	Lys	Met
1			5					10						15	
Asp	Pro	Glu	Leu	Glu	Lys	Lys	Pro	Lys	Glu	Asn	Lys	Ile	Ser	Leu	Glu
		20						25					30		
Ser	Glu	Tyr	Glu	Gly	Ser	Ile	Cys								
	35						40								

<210> 188
 <211> 88
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -33...-1
 <400> 188

Met	Ser	Gln	Thr	Ala	Trp	Leu	Ser	Leu	Leu	Ser	Ser	Ser	Pro	Phe	Gly
		-30					-25						-20		
Pro	Phe	Ser	Ala	Leu	Thr	Phe	Leu	Phe	Leu	His	Leu	Pro	Pro	Ser	Thr
	-15					-10				-5					
Ser	Leu	Phe	Ile	Asn	Leu	Ala	Arg	Gly	Gln	Ile	Lys	Gly	Pro	Leu	Gly
1				5					10					15	
Leu	Ile	Leu	Leu	Leu	Ser	Phe	Cys	Gly	Gly	Tyr	Thr	Lys	Cys	Asp	Phe
			20					25						30	
Ala	Leu	Ser	Tyr	Leu	Glu	Ile	Pro	Asn	Arg	Ile	Glu	Phe	Ser	Ile	Met
		35						40					45		
Asp	Pro	Lys	Arg	Lys	Thr	Lys	Cys								
	50						55								

<210> 189
 <211> 106
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -32...-1
 <400> 189

Met	Phe	Ala	Pro	Ala	Val	Thr	Arg	Ala	Phe	Arg	Lys	Asn	Lys	Thr	Leu
		-30					-25					-20			
Gly	Tyr	Gly	Val	Pro	Met	Leu	Leu	Leu	Ile	Val	Gly	Gly	Ser	Phe	Gly
	-15					-10				-5					
Leu	Arg	Glu	Phe	Ser	Gln	Ile	Arg	Tyr	Asp	Ala	Val	Lys	Ser	Lys	Met
1			5					10						15	
Asp	Pro	Glu	Leu	Glu	Lys	Lys	Leu	Lys	Glu	Asn	Lys	Ile	Ser	Leu	Glu
		20						25					30		
Ser	Glu	Tyr	Glu	Lys	Ile	Lys	Asp	Ser	Lys	Phe	Asp	Asp	Trp	Lys	Asn
	35					40					45				
Ile	Arg	Gly	Pro	Arg	Pro	Trp	Glu	Asp	Pro	Asp	Leu	Leu	Gln	Gly	Arg
	50					55					60				
Asn	Pro	Glu	Ser	Leu	Lys	Thr	Lys	Thr	Thr						
65					70										

<210> 190
 <211> 267
 <212> PRT

321

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -21...-1

<400> 190

Met	Trp	Trp	Phe	Gln	Gln	Gly	Leu	Ser	Phe	Leu	Pro	Ser	Ala	Leu	Val	
-20						-15					-10					
Ile	Trp	Thr	Ser	Ala	Ala	Phe	Ile	Phe	Ser	Tyr	Ile	Thr	Ala	Val	Thr	
-5					1				5					10		
Leu	His	His	Ile	Asp	Pro	Ala	Leu	Pro	Tyr	Ile	Ser	Asp	Thr	Gly	Thr	
			15					20					25			
Val	Ala	Pro	Glu	Lys	Cys	Leu	Phe	Gly	Ala	Met	Leu	Asn	Ile	Ala	Ala	
		30					35					40				
Val	Leu	Cys	Ile	Ala	Thr	Ile	Tyr	Val	Arg	Tyr	Lys	Gln	Val	His	Ala	
	45					50					55					
Leu	Ser	Pro	Glu	Glu	Asn	Val	Ile	Ile	Lys	Leu	Asn	Lys	Ala	Gly	Leu	
60					65					70					75	
Val	Leu	Gly	Ile	Leu	Ser	Cys	Leu	Gly	Leu	Ser	Ile	Val	Ala	Asn	Phe	
				80					85					90		
Gln	Lys	Thr	Thr	Leu	Phe	Ala	Ala	His	Val	Ser	Gly	Ala	Val	Leu	Thr	
			95					100						105		
Phe	Gly	Met	Gly	Ser	Leu	Tyr	Met	Phe	Val	Gln	Thr	Ile	Leu	Ser	Tyr	
		110					115					120				
Gln	Met	Gln	Pro	Lys	Ile	His	Gly	Lys	Gln	Val	Phe	Trp	Ile	Arg	Leu	
	125					130					135					
Leu	Leu	Val	Ile	Trp	Cys	Gly	Val	Ser	Ala	Leu	Ser	Met	Leu	Thr	Cys	
140					145					150					155	
Ser	Ser	Val	Leu	His	Ser	Gly	Asn	Phe	Gly	Thr	Asp	Leu	Glu	Gln	Lys	
				160					165					170		
Leu	His	Trp	Asn	Pro	Glu	Asp	Lys	Gly	Tyr	Ala	Leu	His	Met	Ile	Thr	
		175						180					185			
Thr	Ala	Ala	Glu	Trp	Ser	Met	Ser	Phe	Ser	Phe	Phe	Gly	Phe	Phe	Leu	
		190					195					200				
Thr	Tyr	Ile	Arg	Asp	Phe	Gln	Lys	Ile	Ser	Leu	Arg	Val	Glu	Ala	Asn	
	205					210					215					
Leu	His	Gly	Leu	Thr	Leu	Tyr	Asp	Thr	Ala	Pro	Cys	Pro	Ile	Asn	Asn	
220					225					230					235	
Glu	Arg	Thr	Arg	Leu	Leu	Ser	Arg	Asp	Ile	Arg						
				240					245							

<210> 191

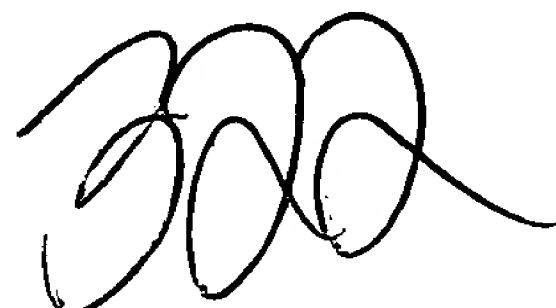
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<212> PRT

<213> Homo sapiens

<400> 191

Met	Gly	Cys	Val	Phe	Gln	Ser	Thr	Glu	Asp	Lys	Cys	Ile	Phe	Lys	Ile	
1				5					10					15		
Asp	Trp	Thr	Leu	Ser	Pro	Gly	Glu	His	Ala	Lys	Asp	Glu	Tyr	Val	Leu	
			20					25					30			
Tyr	Tyr	Tyr	Ser	Asn	Leu	Ser	Val	Pro	Ile	Gly	Arg	Phe	Gln	Asn	Arg	
		35					40					45				
Val	His	Leu	Met	Gly	Asp	Ile	Leu	Cys	Asn	Asp	Gly	Ser	Leu	Leu	Leu	
	50					55				60						
Gln	Asp	Val	Gln	Glu	Ala	Asp	Gln	Gly	Thr	Tyr	Ile	Cys	Glu	Ile	Arg	
65					70					75					80	
Leu	Lys	Gly	Glu	Ser	Gln	Val	Phe	Lys	Lys	Ala	Val	Val	Leu	His	Val	
				85					90					95		
Leu	Pro	Glu	Glu	Pro	Lys	Gly	Thr	Gln	Met	Leu	Thr					





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100

105

<210> 192
 <211> 69
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 <213> Homo sapiens
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 <222> -46...-1
 <400> 192

Met	Ser	Val	Phe	Trp	Gly	Phe	Val	Gly	Phe	Leu	Val	Pro	Trp	Phe	Ile
	-45					-40					-35				
Pro	Lys	Gly	Pro	Asn	Arg	Gly	Val	Ile	Ile	Thr	Met	Leu	Val	Thr	Cys
-30					-25					-20					-15
Ser	Val	Cys	Cys	Tyr	Leu	Phe	Trp	Leu	Ile	Ala	Ile	Leu	Ala	Gln	Leu
				-10					-5					1	
Asn	Pro	Leu	Phe	Gly	Pro	Gln	Leu	Lys	Asn	Glu	Thr	Ile	Trp	Tyr	Leu
	5						10					15			
Lys	Tyr	His	Trp	Pro											
	20														

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 <221> SIGNAL
 <222> -28...-1
 <400> 193

Met	Trp	Arg	Leu	Leu	Ala	Arg	Ala	Ser	Ala	Pro	Leu	Leu	Arg	Val	Pro
			-25					-20					-15		
Leu	Ser	Asp	Ser	Trp	Ala	Leu	Leu	Pro	Ala	Ser	Ala	Gly	Val	Lys	Thr
		-10					-5					1			
Leu	Leu	Pro	Val	Pro	Ser	Phe	Glu	Asp	Val	Ser	Ile	Pro	Glu	Lys	Pro
5					10				15						20
Lys	Leu	Arg	Phe	Ile	Glu	Arg	Ala	Pro	Leu	Val	Pro	Lys	Val	Arg	Arg
			25					30						35	
Glu	Pro	Lys	Asn	Leu	Ser	Asp	Ile	Arg	Gly	Pro	Ser	Thr	Glu	Ala	Thr
			40					45					50		
Glu	Phe	Thr	Glu	Gly	Asn	Phe	Ala	Ile	Leu	Ala	Leu	Gly	Gly	Gly	Tyr
	55					60						65			
Leu	His	Trp	Gly	His	Phe	Glu	Met	Met	Arg	Leu	Thr	Ile	Asn	Arg	Ser
	70				75						80				
Met	Asp	Pro	Lys	Asn	Met	Phe	Ala	Ile	Trp	Arg	Val	Pro	Ala	Pro	Phe
85				90					95						100
Lys	Pro	Ile	Thr	Arg	Lys	Ser	Val	Gly	His	Arg	Met	Gly	Gly	Gly	Lys
				105					110					115	
Gly	Ala	Ile	Asp	His	Tyr	Val	Thr	Pro	Val	Lys	Ala	Gly	Arg	Leu	Val
			120					125					130		
Val	Glu	Met	Gly	Gly	Arg	Cys	Glu	Phe	Glu	Glu	Val	Gln	Gly	Phe	Leu
		135				140						145			
Asp	Gln	Val	Ala	His	Lys	Leu	Pro	Phe	Ala	Ala	Lys	Ala	Val	Ser	Arg
	150					155					160				
Gly	Thr	Leu	Glu	Lys	Met	Arg	Lys	Asp	Gln	Glu	Glu	Arg	Glu	Arg	Asn
165					170				175						180
Asn	Gln	Asn	Pro	Trp	Thr	Phe	Glu	Arg	Ile	Ala	Thr	Ala	Asn	Met	Leu
				185					190					195	
Gly	Ile	Arg	Lys	Val	Leu	Ser	Pro	Tyr	Asp	Leu	Thr	His	Lys	Gly	Lys


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195

324

Leu

<210> 198
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Met	Ala	Ser	Lys	Ile	Leu	Leu	Asn	Val	Gln	Glu	Glu	Val	Thr	Cys	Pro	
		-35					-30					-25				
Ile	Cys	Leu	Glu	Leu	Leu	Thr	Glu	Pro	Leu	Ser	Leu	Asp	Cys	Gly	His	
	-20					-15					-10					
Ser	Leu	Cys	Arg	Ala	Cys	Ile	Thr	Val	Ser	Asn	Lys	Glu	Ala	Val	Thr	
-5					1			5						10		
Ser	Met	Gly	Gly	Lys	Ser	Ser	Cys	Pro	Val	Cys	Gly	Ile	Ser	Tyr	Ser	
		15					20					25				
Phe	Glu	His	Leu	Gln	Ala	Asn	Gln	His	Leu	Ala	Asn	Ile	Val	Glu	Arg	
	30					35						40				
Leu	Lys	Glu	Val	Lys	Leu	Ser	Pro	Asp	Asn	Gly	Lys	Lys	Arg	Asp	Leu	
	45					50					55					
Cys	Asp	His	His	Gly	Glu	Lys	Leu	Leu	Leu	Phe	Cys	Lys	Glu	Asp	Arg	
60					65					70					75	
Lys	Val	Ile	Cys	Trp	Leu	Cys	Glu	Arg	Ser	Gln	Glu	His	Arg	Gly	His	
				80				85						90		
His	Thr	Val	Leu	Thr	Glu	Glu	Val	Phe	Lys	Glu	Cys	Gln	Glu	Lys	Leu	
		95						100					105			
Gln	Ala	Val	Leu	Lys	Arg	Leu	Lys	Lys	Glu	Glu	Glu	Glu	Ala	Glu	Lys	
	110					115						120				
Leu	Glu	Ala	Asp	Ile	Arg	Glu	Glu	Lys	Thr	Ser	Trp	Lys	Tyr	Gln	Val	
	125					130					135					
Gln	Thr	Glu	Arg	Gln	Arg	Ile	Gln	Thr	Glu	Phe	Asp	Gln	Leu	Arg	Ser	
140					145					150					155	
Ile	Leu	Asn	Asn	Glu	Glu	Gln	Arg	Glu	Leu	Gln	Arg	Leu	Glu	Glu	Glu	
				160				165						170		
Glu	Lys	Lys	Thr	Leu	Asp	Lys	Phe	Ala	Glu	Ala	Glu	Asp	Glu	Leu	Val	
			175					180					185			
Gln	Gln	Lys	Gln	Leu	Val	Arg	Glu	Leu	Ile	Ser	Asp	Val	Glu	Cys	Arg	
		190					195					200				
Ser	Gln	Trp	Ser	Thr	Met	Glu	Leu	Leu	Gln	Asp	Met	Ser	Gly	Ile	Met	
	205					210				215						
Lys	Trp	Ser	Glu	Ile	Trp	Arg	Leu	Lys	Lys	Pro	Lys	Met	Val	Ser	Lys	
220					225					230					235	
Lys	Leu	Lys	Thr	Val	Phe	His	Ala	Pro	Asp	Leu	Ser	Arg	Met	Leu	Gln	
				240					245					250		
Met	Phe	Arg	Glu	Leu	Thr	Ala	Val	Arg	Cys	Tyr	Trp	Val	Asp	Val	Thr	
		255						260					265			
Leu	Asn	Ser	Val	Asn	Leu	Asn	Leu	Asn	Leu	Val	Leu	Ser	Glu	Asp	Gln	
		270				275						280				
Arg	Gln	Val	Ile	Ser	Val	Pro	Ile	Trp	Pro	Phe	Gln	Cys	Tyr	Asn	Tyr	
	285					290					295					
Gly	Val	Leu	Gly	Ser	Gln	Tyr	Phe	Ser	Ser	Gly	Lys	His	Tyr	Trp	Glu	
300					305					310					315	
Val	Asp	Val	Ser	Lys	Lys	Thr	Ala	Trp	Ile	Leu	Gly	Val	Tyr	Cys	Arg	
				320					325					330		
Thr	Tyr	Ser	Arg	His	Met	Lys	Tyr	Val	Val	Arg	Arg	Cys	Ala	Asn	Arg	
			335					340					345			

Gln	Asn	Leu	Tyr	Thr	Lys	Tyr	Arg	Pro	Leu	Phe	Gly	Tyr	Trp	Val	Ile
		350					355					360			
Gly	Leu	Gln	Asn	Lys	Cys	Lys	Tyr	Gly	Ala	Lys	Lys	Lys			
	365					370					375				

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Met	Arg	Thr	Leu	Phe	Asn	Leu	Leu	Trp	Leu	Ala	Leu	Ala	Cys	Ser	Pro
				-15					-10					-5	
Val	His	Thr	Thr	Leu	Ser	Lys	Ser	Asp	Ala	Lys	Lys	Ala	Ala	Ser	Lys
		1				5					10				
Thr	Leu	Leu	Glu	Lys	Ser	Gln	Phe	Ser	Asp	Lys	Pro	Val	Gln	Asp	Arg
	15					20					25				
Gly	Leu	Val	Val	Thr	Asp	Leu	Lys	Ala	Glu	Ser	Val	Val	Leu	Glu	His
30					35				40					45	
Arg	Ser	Tyr	Cys	Ser	Ala	Lys	Ala	Arg	Asp	Arg	His	Phe	Ala	Gly	Asp
				50					55					60	
Val	Leu	Gly	Tyr	Val	Thr	Pro	Trp	Asn	Ser	His	Gly	Tyr	Asp	Val	Thr
		65					70					75			
Lys	Val	Phe	Gly	Ser	Lys	Phe	Thr	Gln	Ile	Ser	Pro	Val	Trp	Leu	Gln
		80				85					90				
Leu	Lys	Arg	Arg	Gly	Arg	Glu	Met	Phe	Glu	Val	Thr	Gly	Leu	His	Asp
	95					100					105				
Val	Asp	Gln	Gly	Trp	Met	Arg	Ala	Val	Arg	Lys	His	Ala	Lys	Gly	Leu
110					115					120					125
His	Ile	Val	Pro	Arg	Leu	Leu	Phe	Glu	Asp	Trp	Thr	Tyr	Asp	Asp	Phe
				130					135					140	
Arg	Asn	Val	Leu	Asp	Ser	Glu	Asp	Glu	Ile	Glu	Glu	Leu	Ser	Lys	Thr
		145						150					155		
Val	Val	Gln	Val	Ala	Lys	Asn	Gln	His	Phe	Asp	Gly	Phe	Val	Val	Glu
		160					165					170			
Val	Trp	Asn	Gln	Leu	Leu	Ser	Gln	Lys	Arg	Val	Gly	Leu	Ile	His	Met
	175					180					185				
Leu	Thr	His	Leu	Ala	Glu	Ala	Leu	His	Gln	Ala	Arg	Leu	Leu	Ala	Leu
190					195					200					205
Leu	Val	Ile	Pro	Pro	Ala	Ile	Thr	Pro	Gly	Thr	Asp	Gln	Leu	Gly	Met
				210					215					220	
Phe	Thr	His	Lys	Glu	Phe	Glu	Gln	Leu	Ala	Pro	Val	Leu	Asp	Gly	Phe
		225					230						235		
Ser	Leu	Met	Thr	Tyr	Asp	Tyr	Ser	Thr	Ala	His	Gln	Pro	Gly	Pro	Asn
	240					245						250			
Ala	Pro	Leu	Ser	Trp	Val	Arg	Ala	Cys	Val	Gln	Val	Leu	Asp	Pro	Lys
	255					260					265				
Ser	Lys	Trp	Arg	Ser	Lys	Ile	Leu	Leu	Gly	Leu	Asn	Phe	Tyr	Gly	Met
270					275					280					285
Asp	Tyr	Ala	Thr	Ser	Lys	Asp	Ala	Arg	Glu	Pro	Val	Val	Gly	Ala	Arg
				290					295					300	
Tyr	Ile	Gln	Thr	Leu	Lys	Asp	His	Arg	Pro	Arg	Met	Val	Trp	Asp	Ser
		305					310						315		
Gln	Ala	Ser	Glu	His	Phe	Phe	Glu	Tyr	Lys	Lys	Ser	Arg	Ser	Gly	Arg
	320						325					330			
His	Val	Val	Phe	Tyr	Pro	Thr	Leu	Lys	Ser	Leu	Gln	Val	Arg	Leu	Glu

327

335		340		345
Leu Ala Arg Glu Leu Gly Val Gly Val Ser Ile Trp Glu Leu Gly Gln				
350		355		360
Gly Leu Asp Tyr Phe Tyr Asp Leu Leu				365
	370			

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Met Leu Leu Ser Ile Gly Met Leu Met Leu Ser Ala Thr Gln Val Tyr	
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Thr Val Leu Thr Val Gln Leu Phe Ala Phe Leu Asn Pro Leu Pro Val	
5 10 15	
Glu Ala Asp Ile Leu Ala Tyr Asn Phe Glu Asn Ala Ser Gln Thr Phe	
20 25 30 35	
Asp Asp Leu Pro Ala Arg Phe Gly Tyr Arg Leu Pro Ala Glu Gly Leu	
	40 45 50
Lys Gly Phe Leu Ile Asn Ser Lys Pro Glu Asn Ala Cys Glu Pro Ile	
	55 60 65
Val Pro Pro Pro Val Lys Asp Asn Ser Ser Gly Thr Phe Ile Val Leu	
	70 75 80
Ile Arg Arg Leu Asp Cys Asn Phe Asp Ile Lys Val Leu Asn Ala Gln	
	85 90 95
Arg Ala Gly Tyr Lys Ala Ala Ile Val His Asn Val Asp Ser Asp Asp	
100 105 110 115	
Leu Ile Ser Met Gly Ser Asn Asp Ile Glu Val Leu Lys Lys Ile Asp	
	120 125 130
Ile Pro Ser Val Phe Ile Gly Glu Ser Ser Ala Ser Ser Leu Lys Asp	
	135 140 145
Glu Phe Thr Tyr Glu Lys Gly Gly His Leu Ile Leu Val Pro Glu Phe	
	150 155 160
Ser Leu Pro Leu Glu Tyr Tyr Leu Ile Pro Phe Leu Ile Ile Val Gly	
	165 170 175
Ile Cys Leu Ile Leu Ile Val Ile Phe Met Ile Thr Lys Phe Val Gln	
180 185 190 195	
Asp Arg His Arg Ala Arg Arg Asn Arg Leu Arg Lys Asp Gln Leu Lys	
	200 205 210
Lys Leu Pro Val His Lys Phe Lys Lys Gly Asp Glu Tyr Asp Val Cys	
	215 220 225
Ala Ile Cys Leu Asp Glu Tyr Glu Asp Gly Asp Lys Leu Arg Ile Leu	
	230 235 240
Pro Cys Ser His Ala Tyr His Cys Lys Cys Val Asp Pro Trp Leu Thr	
	245 250 255
Lys Thr Lys Lys Thr Cys Pro Val Cys Arg Gln Lys Val Val Pro Ser	
260 265 270 275	
Gln Gly Asp Ser Asp Ser Asp Thr Asp Ser Ser Gln Glu Glu Asn Glu	
	280 285 290
Val Thr Glu His Thr Pro Leu Leu Arg Pro Leu Ala Ser Val Ser Ala	
	295 300 305
Gln Ser Phe Gly Ala Leu Ser Glu Ser Arg Ser His Gln Asn Met Thr	
	310 315 320
Glu Ser Ser Asp Tyr Glu Glu Asp Asp Asn Glu Asp Thr Asp Ser Ser	
	325 330 335



Asp Ala Glu Asn Glu Ile Asn Glu His Asp Val Val Val Gln Leu Gln
 340 345 350 355
 Pro Asn Gly Glu Arg Asp Tyr Asn Ile Ala Asn Thr Val
 360 365

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<221> SIGNAL
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 <400> 201

Met Asp Ser Arg Val Ser Ser Pro Glu Lys Gln Asp Lys Glu Asn Phe
 -40 -35 -30
 Val Gly Val Asn Asn Lys Arg Leu Gly Val Cys Gly Trp Ile Leu Phe
 -25 -20 -15
 Ser Leu Ser Phe Leu Leu Val Ile Ile Thr Phe Pro Ile Ser Ile Trp
 -10 -5 1 5
 Met Cys Leu Lys Ile Ile Arg Glu Tyr Glu Arg Ala Val Val Phe Arg
 10 15 20
 Leu Gly Arg Ile Gln Ala Asp Lys Ala Lys Gly Pro Gly Leu Ile Leu
 25 30 35
 Val Leu Pro Cys Ile Asp Val Phe Val Lys Val Asp Leu Arg Thr Val
 40 45 50
 Thr Cys Asn Ile Pro Pro Gln Glu Ile Leu Thr Arg Asp Ser Val Thr
 55 60 65 70
 Thr Gln Val Asp Gly Val Val Tyr Tyr Arg Ile Tyr Ser Ala Val Ser
 75 80 85
 Ala Val Ala Asn Val Asn Asp Val His Gln Ala Thr Phe Leu Leu Ala
 90 95 100
 Gln Thr Thr Leu Arg Asn Val Leu Gly Thr Gln Thr Leu Ser Gln Ile
 105 110 115
 Leu Ala Gly Arg Glu Glu Ile Ala His Ser Ile Gln Thr Leu Leu Asp
 120 125 130
 Asp Ala Thr Glu Leu Trp Gly Ile Arg Val Ala Arg Val Glu Ile Lys
 135 140 145 150
 Asp Val Arg Ile Pro Val Gln Leu Gln Arg Ser Met Ala Ala Glu Ala
 155 160 165
 Glu Ala Thr Arg Glu Ala Arg Ala Lys Val Leu Ala Ala Glu Gly Glu
 170 175 180
 Met Ser Ala Ser Lys Ser Leu Lys Ser Ala Ser Met Val Leu Ala Glu
 185 190 195
 Ser Pro Ile Ala Leu Gln Leu Arg Tyr Leu Gln Thr Leu Ser Thr Val
 200 205 210
 Ala Thr Glu Lys Asn Ser Thr Ile Val Phe Pro Leu Pro Met Asn Ile
 215 220 225 230
 Leu Glu Gly Ile Gly Gly Val Ser Tyr Asp Asn His Lys Lys Leu Pro
 235 240 245
 Asn Lys Ala

<210> 202
 <211> 92
 <212> PRT
 <213> Homo sapiens
 <400> 202

Met Pro Pro Arg Asn Leu Leu Glu Leu Leu Ile Asn Ile Lys Ala Gly
 1 5 10 15

329

Thr	Tyr	Leu	Pro	Gln	Ser	Tyr	Leu	Ile	His	Glu	His	Met	Val	Ile	Thr
		20					25					30			
Asp	Arg	Ile	Glu	Asn	Ile	Asp	His	Leu	Gly	Phe	Phe	Ile	Tyr	Arg	Leu
		35				40						45			
Cys	His	Asp	Lys	Glu	Thr	Tyr	Lys	Leu	Gln	Arg	Arg	Glu	Thr	Ile	Lys
	50					55					60				
Gly	Ile	Gln	Lys	Arg	Glu	Ala	Ser	Asn	Cys	Phe	Ala	Ile	Arg	His	Phe
65					70					75					80
Glu	Asn	Lys	Phe	Ala	Val	Glu	Thr	Leu	Ile	Cys	Ser				
			85					90							

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 <213> Homo sapiens
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 <221> SIGNAL
 <222> -63...-1
 <400> 203

Met	Ser	Ala	Ala	Gly	Ala	Arg	Gly	Leu	Arg	Ala	Thr	Tyr	His	Arg	Leu
		-60					-55						-50		
Pro	Asp	Lys	Val	Glu	Leu	Met	Leu	Pro	Glu	Lys	Leu	Arg	Pro	Leu	Tyr
		-45				-40						-35			
Asn	His	Pro	Ala	Gly	Pro	Arg	Thr	Val	Phe	Phe	Trp	Ala	Pro	Ile	Met
	-30					-25					-20				
Lys	Trp	Gly	Leu	Val	Cys	Ala	Gly	Leu	Ala	Asp	Met	Ala	Arg	Pro	Ala
-15				-10					-5						1
Glu	Lys	Leu	Ser	Thr	Ala	Gln	Ser	Ala	Val	Leu	Met	Ala	Thr	Gly	Phe
		5					10					15			
Ile	Trp	Ser	Arg	Tyr	Ser	Leu	Val	Ile	Ile	Pro	Lys	Asn	Trp	Ser	Leu
	20					25					30				
Phe	Ala	Val	Asn	Phe	Phe	Val	Gly	Ala	Ala	Gly	Ala	Ser	Gln	Leu	Phe
	35					40					45				
Arg	Ile	Trp	Arg	Tyr	Asn	Gln	Glu	Leu	Lys	Ala	Lys	Ala	His	Lys	
50					55					60					

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 <211> 84
 <212> PRT
 <213> Homo sapiens
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 <221> SIGNAL
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 <400> 204

Met	Lys	Gly	Trp	Gly	Trp	Leu	Ala	Leu	Leu	Leu	Gly	Ala	Leu	Leu	Gly
-20					-15					-10					-5
Thr	Ala	Trp	Ala	Arg	Arg	Ser	Gln	Asp	Leu	His	Cys	Gly	Ala	Cys	Arg
			1				5					10			
Ala	Leu	Val	Asp	Glu	Leu	Glu	Trp	Glu	Ile	Ala	Gln	Val	Asp	Pro	Lys
	15					20					25				
Lys	Thr	Ile	Gln	Met	Gly	Ser	Phe	Arg	Ile	Asn	Pro	Asp	Gly	Ser	Gln
30					35					40					
Ser	Val	Val	Glu	Val	Thr	Val	Thr	Val	Pro	Pro	Asn	Lys	Val	Ala	His
45					50					55					60
Ser	Gly	Phe	Gly												

<210> 205
 <211> 182

<212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -20...-1
 <400> 205
 Met Lys Gly Trp Gly Trp Leu Ala Leu Leu Leu Gly Ala Leu Leu Gly
 -20 -15 -10 -5
 Thr Ala Trp Ala Arg Arg Ser Gln Asp Leu His Cys Gly Ala Cys Arg
 1 5 10
 Ala Leu Val Asp Glu Leu Glu Trp Glu Ile Ala Gln Val Asp Pro Lys
 15 20 25
 Lys Thr Ile Gln Met Gly Ser Phe Arg Ile Asn Pro Asp Gly Ser Gln
 30 35 40
 Ser Val Val Glu Val Pro Tyr Ala Arg Ser Glu Ala His Leu Thr Glu
 45 50 55 60
 Leu Leu Glu Glu Ile Cys Asp Arg Met Lys Glu Tyr Gly Glu Gln Ile
 65 70 75
 Asp Pro Ser Thr His Arg Lys Asn Tyr Val Arg Val Val Gly Arg Asn
 80 85 90
 Gly Glu Ser Ser Glu Leu Asp Leu Gln Gly Ile Arg Ile Asp Ser Asp
 95 100 105
 Ile Ser Gly Thr Leu Lys Phe Ala Cys Gly Ser Ile Val Glu Glu Tyr
 110 115 120
 Glu Asp Glu Leu Ile Glu Phe Phe Ser Arg Glu Ala Asp Asn Val Lys
 125 130 135 140
 Asp Lys Leu Cys Ser Lys Arg Thr Asp Leu Cys Asp His Ala Leu His
 145 150 155
 Ile Ser His Asp Glu Leu
 160

<210> 206
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 Met Pro Ala Gly Val Pro Met Ser Thr Tyr Leu Lys Met Phe Ala Ala
 -25 -20 -15 -10
 Ser Leu Leu Ala Met Cys Ala Gly Ala Glu Val Val His Arg Tyr Tyr
 -5 1 5
 Arg Pro Asp Leu Thr Ile Pro Glu Ile Pro Pro Lys Arg Gly Glu Leu
 10 15 20
 Lys Thr Glu Leu Leu Gly Leu Lys Glu Arg Lys His Lys Pro Gln Val
 25 30 35
 Ser Gln Gln Glu Glu Leu Lys
 40 45

<210> 207
 <211> 73
 <212> PRT
 <213> Homo sapiens
 <400> 207
 Met Arg Ile Arg Met Thr Asp Gly Arg Thr Leu Val Gly Cys Phe Leu
 1 5 10 15
 Cys Thr Asp Arg Asp Cys Asn Val Ile Leu Gly Ser Ala Gln Glu Phe

331

	20		25		30										
Leu	Lys	Pro	Ser	Asp	Ser	Phe	Ser	Ala	Gly	Glu	Pro	Arg	Val	Leu	Gly
	35		40		45										
Leu	Ala	Met	Val	Pro	Gly	His	His	Ile	Val	Ser	Ile	Glu	Val	Gln	Arg
	50		55		60										
Glu	Ser	Leu	Thr	Gly	Pro	Pro	Tyr	Leu							
65					70										

<210> 208

<211> 169

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -150..-1

<220>

<221> UNSURE

<222> -67

<223> Xaa = any one of the twenty amino acids

<400> 208

Met	Ala	Glu	Thr	Lys	Asp	Thr	Ala	Gln	Met	Leu	Val	Thr	Phe	Lys	Asp
-150					-145					-140					-135
Val	Ala	Val	Thr	Phe	Thr	Arg	Glu	Glu	Trp	Arg	Gln	Leu	Asp	Leu	Ala
				-130					-125						-120
Gln	Arg	Thr	Leu	Tyr	Arg	Glu	Gly	Ile	Gly	Phe	Pro	Lys	Pro	Glu	Leu
			-115					-110					-105		
Val	His	Leu	Leu	Glu	His	Gly	Gln	Glu	Leu	Trp	Ile	Val	Lys	Arg	Gly
		-100				-95						-90			
Leu	Ser	His	Ala	Thr	Cys	Ala	Glu	Phe	His	Ser	Cys	Cys	Pro	Gly	Trp
-85					-80					-75					
Ser	Ala	Val	Xaa	Arg	His	Leu	Ser	Ser	Leu	Gln	Leu	Leu	Pro	Pro	Glu
-70				-65						-60					-55
Phe	Lys	Gly	Phe	Ser	Cys	Leu	Ser	Leu	Pro	Ser	Ser	Trp	Asp	Tyr	Arg
			-50					-45						-40	
Arg	Pro	Pro	Pro	Cys	Pro	Ala	Gly	Phe	Phe	Val	Phe	Leu	Val	Glu	Thr
			-35				-30						-25		
Gly	Leu	His	His	Val	Gly	Gln	Ala	Gly	Leu	Glu	Leu	Leu	Thr	Ser	Cys
		-20				-15						-10			
Ser	Pro	Pro	Ala	Ser	Ala	Ser	Gln	Ser	Ala	Ala	Ile	Thr	Gly	Val	Ser
-5					1				5						10
His	Arg	Ala	Arg	Gln	Arg	Lys	Thr	Ala							
				15											

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<211> 76

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -22..-1

<400> 209

Met	Glu	Leu	Ile	Ser	Pro	Thr	Val	Ile	Ile	Ile	Leu	Gly	Cys	Leu	Ala
	-20						-15					-10			
Leu	Phe	Leu	Leu	Leu	Gln	Arg	Lys	Asn	Leu	Arg	Arg	Pro	Pro	Cys	Ile
-5					1				5						10
Lys	Gly	Trp	Ile	Pro	Trp	Ile	Gly	Val	Gly	Phe	Glu	Phe	Gly	Lys	Ala
			15				20						25		
Pro	Leu	Glu	Phe	Ile	Glu	Lys	Ala	Arg	Ile	Lys	Val	Cys	Gly	Arg	Gly

332

Arg Arg Gly Leu Gln Arg Arg Gln Cys Phe Leu Phe
 30 35 40
 45 50

<210> 210
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Met Ala Glu Thr Lys Asp Ala Ala Gln Met Leu Val Thr Phe Lys Asp
 -50 -45 -40
 Val Ala Val Thr Phe Thr Arg Glu Glu Trp Arg Gln Leu Asp Leu Ala
 -35 -30 -25
 Gln Arg Thr Leu Tyr Arg Glu Val Met Leu Glu Thr Cys Gly Leu Leu
 -20 -15 -10
 Val Ser Leu Val Glu Ser Ile Trp Leu His Ile Thr Glu Asn Gln Ile
 -5 1 5 10
 Lys Leu Ala Ser Pro Gly Arg Lys Phe Thr Asn Ser Pro Asp Glu Lys
 15 20 25
 Pro Glu Val Trp Leu Ala Pro Gly Leu Phe Gly Ala Ala Ala Gln
 30 35 40

<210> 211
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 <400> 211

Met Glu Leu Ile Ser Pro Thr Val Ile Ile Ile Leu Gly Cys Leu Ala
 -20 -15 -10
 Leu Phe Leu Leu Leu Gln Arg Lys Asn Leu Arg Arg Pro Pro Cys Ile
 -5 1 5 10
 Lys Gly Trp Ile Pro Trp Ile Gly Val Gly Phe Glu Phe Gly Lys Ala
 15 20 25
 Pro Leu Glu Phe Ile Glu Lys Ala Arg Ile Lys Tyr Gly Pro Ile Phe
 30 35 40
 Thr Val Phe Ala Met Gly Asn Arg Met Thr Phe Val Thr Glu Glu Glu
 45 50 55
 Gly Ile Asn Val Phe Leu Lys Ser Lys Lys Lys Lys
 60 65 70

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 <222> -16...-1
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Met Ile Ile Ser Leu Phe Ile Tyr Ile Phe Leu Thr Cys Ser Asn Thr
 -15 -10 -5
 Ser Pro Ser Tyr Gln Gly Thr Gln Leu Gly Leu Gly Leu Pro Ser Ala
 1 5 10 15

333

Gln	Trp	Trp	Pro	Leu	Thr	Gly	Arg	Arg	Met	Gln	Cys	Cys	Arg	Leu	Phe
			20					25					30		
Cys	Phe	Leu	Leu	Gln	Asn	Cys	Leu	Phe	Pro	Phe	Pro	Leu	His	Leu	Ile
		35					40					45			
Gln	His	Asp	Pro	Cys	Glu	Leu	Val	Leu	Thr	Ile	Ser	Trp	Asp	Trp	Ala
	50					55					60				
Glu	Ala	Gly	Ala	Ser	Leu	Tyr	Ser	Pro							
65					70										

<210> 213
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Met	Lys	Val	Asp	Lys	Asp	Arg	Gln	Met	Val	Val	Leu	Glu	Glu	Glu	Phe
1				5				10						15	
Arg	Asn	Ile	Ser	Pro	Glu	Glu	Leu	Lys	Met	Glu	Leu	Pro	Glu	Arg	Gln
			20					25					30		
Pro	Arg	Phe	Val	Val	Tyr	Ser	Tyr	Lys	Tyr	Val	Arg	Asp	Asp	Gly	Arg
		35					40					45			
Val	Ser	Tyr	Pro	Leu	Cys	Phe	Ile	Phe	Ser	Ser	Pro	Val	Gly	Cys	Lys
	50					55					60				
Pro	Glu	Gln	Gln	Met	Met	Tyr	Ala	Gly	Ser	Lys	Asn	Arg	Leu	Val	Gln
65				70						75					80
Thr	Ala	Glu	Leu	Thr	Lys	Val	Phe	Glu	Ile	Arg	Thr	Thr	Asp	Asp	Leu
				85					90				95		
Thr	Glu	Ala	Trp	Leu	Gln	Glu	Lys	Leu	Ser	Phe	Phe	Arg			
			100					105							

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 <222> -103...-1
 <400> 214

Met	Val	Ile	Arg	Val	Tyr	Ile	Ala	Ser	Ser	Ser	Gly	Ser	Thr	Ala	Ile
			-100					-95					-90		
Lys	Lys	Lys	Gln	Gln	Asp	Val	Leu	Gly	Phe	Leu	Glu	Ala	Asn	Lys	Ile
		-85					-80					-75			
Gly	Phe	Glu	Glu	Lys	Asp	Ile	Ala	Ala	Asn	Glu	Glu	Asn	Arg	Lys	Trp
	-70					-65					-60				
Met	Arg	Glu	Asn	Val	Pro	Glu	Asn	Ser	Arg	Pro	Ala	Thr	Gly	Asn	Pro
-55				-50					-45					-40	
Leu	Pro	Pro	Gln	Ile	Phe	Asn	Glu	Ser	Gln	Tyr	Arg	Gly	Asp	Tyr	Asp
			-35				-30						-25		
Ala	Phe	Phe	Glu	Ala	Arg	Glu	Asn	Asn	Ala	Val	Tyr	Ala	Phe	Leu	Gly
		-20					-15					-10			
Leu	Thr	Ala	Pro	Ser	Gly	Ser	Lys	Glu	Ala	Glu	Val	Gln	Ala	Lys	Gln
		-5				1				5					
Gln	Ala														
10															

<210> 215
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334

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 <222> -97...-1
 <400> 215
 Met Ala Asp Asp Leu Lys Arg Phe Leu Tyr Lys Lys Leu Pro Ser Val
 -95 -90 -85
 Glu Gly Leu His Ala Ile Val Val Ser Asp Arg Asp Gly Val Pro Val
 -80 -75 -70
 Ile Lys Val Ala Asn Asp Asn Ala Pro Glu His Ala Leu Arg Pro Gly
 -65 -60 -55 -50
 Phe Leu Ser Thr Phe Ala Leu Ala Thr Asp Gln Gly Ser Lys Leu Gly
 -45 -40 -35
 Leu Ser Lys Asn Lys Ser Ile Ile Cys Tyr Tyr Asn Thr Tyr Gln Val
 -30 -25 -20
 Val Gln Phe Asn Arg Leu Pro Leu Val Val Ser Phe Ile Ala Ser Ser
 -15 -10 -5
 Ser Ala Asn Thr Gly Leu Ile Val Ser Leu Glu Lys Glu Leu Ala Pro
 1 5 10 15
 Leu Phe Glu Glu Leu Arg Gln Val Val Glu Val Ser
 20 25

<210> 216
 <211> 93
 <212> PRT
 <213> Homo sapiens
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 <221> SIGNAL
 <222> -22...-1
 <400> 216
 Met Lys Pro Val Leu Pro Leu Gln Phe Leu Val Val Phe Cys Leu Ala
 -20 -15 -10
 Leu Gln Leu Val Pro Gly Ser Pro Lys Gln Arg Val Leu Lys Tyr Ile
 -5 1 5 10
 Leu Glu Pro Pro Pro Cys Ile Ser Ala Pro Glu Asn Cys Thr His Leu
 15 20 25
 Cys Thr Met Gln Glu Asp Cys Glu Lys Gly Phe Gln Cys Cys Ser Ser
 30 35 40
 Phe Cys Gly Ile Val Cys Ser Ser Glu Thr Phe Gln Lys Arg Asn Arg
 45 50 55
 Ile Lys His Lys Gly Ser Glu Val Ile Met Pro Ala Asn
 60 65 70

<210> 217
 <211> 207
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 <222> -42...-1
 <400> 217
 Met His Ile Leu Gln Leu Leu Thr Thr Val Asp Asp Gly Ile Gln Ala
 -40 -35 -30
 Ile Val His Cys Pro Asp Thr Gly Lys Asp Ile Trp Asn Leu Leu Phe
 -25 -20 -15
 Asp Leu Val Cys His Glu Phe Cys Gln Ser Asp Asp Pro Pro Ile Ile
 -10 -5 1 5
 Leu Gln Glu Gln Lys Thr Val Leu Ala Ser Val Phe Ser Val Leu Ser
 10 15 20

Ala	Ile	Tyr	Ala	Ser	Gln	Thr	Glu	Gln	Glu	Tyr	Leu	Lys	Ile	Glu	Lys
	25						30					35			
Val	Asp	Leu	Pro	Leu	Ile	Asp	Ser	Leu	Ile	Arg	Val	Leu	Gln	Asn	Met
	40					45				50					
Glu	Gln	Cys	Gln	Lys	Lys	Pro	Glu	Asn	Ser	Ala	Glu	Ser	Asn	Thr	Glu
55					60					65					70
Glu	Thr	Lys	Arg	Thr	Asp	Leu	Thr	Gln	Asp	Asp	Phe	His	Leu	Lys	Ile
			75						80					85	
Leu	Lys	Asp	Ile	Leu	Cys	Glu	Phe	Leu	Ser	Asn	Ile	Phe	Gln	Ala	Leu
			90					95					100		
Thr	Lys	Glu	Thr	Val	Ala	Gln	Gly	Val	Lys	Glu	Gly	Gln	Leu	Ser	Lys
		105					110					115			
Gln	Lys	Cys	Ser	Ser	Ala	Phe	Gln	Asn	Leu	Leu	Pro	Phe	Tyr	Ser	Pro
	120					125					130				
Val	Val	Glu	Asp	Phe	Ile	Lys	Ile	Leu	Arg	Glu	Val	Asp	Lys	Ala	Leu
135					140					145					150
Ala	Asp	Asp	Leu	Glu	Lys	Asn	Phe	Pro	Ser	Leu	Lys	Val	Gln	Thr	
			155					160						165	

<210> 218
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 <213> Homo sapiens
 <400> 218

Met	Pro	His	Ser	Lys	Pro	Leu	Asp	Trp	Gly	Leu	Ser	Ser	Val	Ala	Glu
1				5					10					15	
Cys	Pro	Ala	Glu	Leu	Phe	Pro	Ser	Thr	Gly	Gly	Leu	Ala	Gly	Lys	Gly
			20					25					30		
Pro	Gly	Leu	Asp	Ile	Leu	Arg	Cys	Val	Leu	Ser	Pro	Trp	Ala	Ser	His
		35					40					45			
Phe	Pro	Ser	Leu	Ser	Leu	Gly	Val	Phe	Asn	Leu					
	50					55									

<210> 219
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 <222> -27...-1
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Met	Asn	Arg	Val	Pro	Ala	Asp	Ser	Pro	Asn	Met	Cys	Leu	Ile	Cys	Leu
		-25					-20					-15			
Leu	Ser	Tyr	Ile	Ala	Leu	Gly	Ala	Ile	His	Ala	Lys	Ile	Cys	Arg	Arg
	-10					-5					1			5	
Ala	Phe	Gln	Glu	Glu	Gly	Arg	Ala	Asn	Ala	Lys	Thr	Gly	Val	Arg	Ala
			10					15						20	
Trp	Cys	Ile	Gln	Pro	Trp	Ala	Lys								
			25												

<210> 220
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336

Met Leu Gln Thr Ser Asn Tyr Ser Leu Val Leu Ser Leu Gln Phe Leu
 -90 -85 -80
 Leu Leu Ser Tyr Asp Leu Phe Val Asn Ser Phe Ser Glu Leu Leu Gln
 -75 -70 -65
 Lys Thr Pro Val Ile Gln Leu Val Leu Phe Ile Ile Gln Asp Ile Ala
 -60 -55 -50
 Val Leu Phe Asn Ile Ile Ile Ile Phe Leu Met Phe Phe Asn Thr Phe
 -45 -40 -35
 Val Phe Gln Ala Gly Leu Val Asn Leu Leu Phe His Lys Phe Lys Gly
 -30 -25 -20 -15
 Thr Ile Ile Leu Thr Ala Val Tyr Phe Ala Leu Ser Ile Ser Leu His
 -10 -5 1
 Val Trp Val Met Asn Leu Arg Trp Lys Asn Ser Asn Ser Phe Ile Trp
 5 10 15
 Thr Asp Gly Leu Gln Met Leu Phe Val Phe Gln Arg Leu Ala Ala Val
 20 25 30
 Leu Tyr Cys Tyr Phe Tyr Lys Arg Thr Ala Val Arg Leu Gly Asp Pro
 35 40 45 50
 His Phe Tyr Gln Asp Ser Leu Trp Leu Arg Lys Glu Phe Met Gln Val
 55 60 65
 Arg Arg

<210> 221
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Met Ala Ser Ala Ser Ala Arg Gly Asn Gln Asp Lys Asp Ala His Phe
 -65 -60 -55
 Pro Pro Pro Ser Lys Gln Ser Leu Leu Phe Cys Pro Lys Ser Lys Leu
 -50 -45 -40
 His Ile His Arg Ala Glu Ile Ser Lys Ile Met Arg Glu Cys Gln Glu
 -35 -30 -25
 Glu Ser Phe Trp Lys Arg Ala Leu Pro Phe Ser Leu Val Ser Met Leu
 -20 -15 -10 -5
 Val Thr Gln Gly Leu Val Tyr Gln Gly Tyr Leu Ala Ala Asn Ser Arg
 1 5 10
 Phe Gly Ser Leu Pro Lys Val Ala Leu Ala Gly Leu Leu Gly Phe Gly
 15 20 25
 Leu Gly Lys Val Ser Tyr Ile Gly Val Cys Gln Ser Lys Phe His Phe
 30 35 40
 Phe Glu Asp Gln Leu Arg Gly Ala Gly Phe Gly Pro Gln His Asn Arg
 45 50 55 60
 His Cys Leu Leu Thr Cys Glu Glu Cys Lys Ile Lys His Gly Leu Ser
 65 70 75
 Glu Lys Gly Asp Ser Gln Pro Ser Ala Ser
 80 85

<210> 222
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 <213> Homo sapiens
 <400> 222

Met Lys Val Glu Glu Glu His Thr Asn Ala Ile Gly Thr Leu His Gly
 1 5 10 15

337

Gly Leu Thr Ala Thr Leu Val Asp Asn Ile Ser Thr Met Ala Leu Leu
 20 25 30
 Cys Thr Glu Arg Gly Ala Pro Gly Val Ser Val Asp Met Asn Ile Thr
 35 40 45
 Tyr Met Ser Pro Ala Lys Leu Gly Glu Asp Ile Val Ile Thr Ala His
 50 55 60
 Val Leu Lys Gln Gly Lys Thr Leu Ala Phe Thr Ser Val Gly Leu Thr
 65 70 75 80
 Asn Lys Ala Thr Gly Lys Leu Ile Ala Gln Gly Arg His Thr Lys His
 85 90 95
 Leu Gly Asn

<210> 223
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Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu
 -20 -15 -10
 Leu Ile Phe Leu Cys Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp Ser
 -5 1 5
 Pro Tyr Phe Lys Met His Lys Pro Val Thr Met
 10 15

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Met Trp Trp Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val
 -20 -15 -10
 Ile Trp Thr Ser Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr
 -5 1 5 10
 Leu His His Ile Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr
 15 20 25
 Val Ala Pro Glu Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala
 30 35 40
 Val Leu Cys Gln Lys
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 <400> 225

Met Ser Pro Gly Ser Ala Leu Ala Leu Leu Trp Ser Leu Pro Ala Ser
 -15 -10 -5
 Asp Leu Gly Arg Ser Val Ile Ala Gly Leu Trp Pro His Thr Gly Val
 1 5 10

338

Leu	Ile	His	Leu	Glu	Thr	Ser	Gln	Ser	Phe	Leu	Gln	Gly	Gln	Leu	Thr
15					20					25					30
Lys	Ser	Ile	Phe	Pro	Leu	Cys	Cys	Thr	Ser	Leu	Phe	Cys	Val	Cys	Val
				35					40					45	
Val	Thr	Val	Gly	Gly	Gly	Arg	Val	Gly	Ser	Thr	Phe	Val	Ala		
			50					55					60		

<210> 226
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Met	Arg	Leu	Pro	Pro	Ala	Leu	Pro	Ser	Gly	Tyr	Thr	Asp	Ser	Thr	Ala
		-45					-40					-35			
Leu	Glu	Gly	Leu	Val	Tyr	Tyr	Leu	Asn	Gln	Lys	Leu	Leu	Phe	Ser	Ser
	-30					-25					-20				
Pro	Ala	Ser	Ala	Leu	Leu	Phe	Phe	Ala	Arg	Pro	Cys	Val	Phe	Cys	Phe
-15					-10				-5						1
Lys	Ala	Ser	Lys	Met	Gly	Pro	Gln	Phe	Glu	Asn	Tyr	Pro	Thr	Phe	Pro
		5					10					15			
Thr	Tyr	Ser	Pro	Leu	Pro	Ile	Ile	Pro	Phe	Gln	Leu	His	Gly	Arg	Phe
		20					25					30			

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Met	Trp	Leu	Asp	Pro	Val	Phe	Pro	Leu	Phe	Pro	Val	Gly	Asp	His	Tyr
			-100					-95					-90		
Leu	Pro	His	Leu	His	Met	Asp	Val	Leu	Glu	Gly	Leu	Ile	Leu	Val	Leu
		-85					-80					-75			
Pro	Cys	Ile	Asp	Val	Phe	Val	Lys	Val	Asp	Leu	Arg	Thr	Val	Thr	Cys
	-70				-65				-60						
Asn	Ile	Pro	Pro	Gln	Glu	Ile	Leu	Thr	Arg	Asp	Ser	Val	Thr	Thr	Gln
-55					-50				-45						-40
Val	Asp	Gly	Val	Val	Tyr	Tyr	Arg	Ile	Tyr	Ser	Ala	Val	Ser	Ala	Val
			-35					-30						-25	
Ala	Asn	Val	Asn	Asp	Val	His	Gln	Ala	Thr	Phe	Leu	Leu	Ala	Gln	Thr
		-20					-15						-10		
Thr	Leu	Arg	Asn	Val	Leu	Gly	Thr	Gln	Thr	Leu	Ser	Gln	Ile	Leu	Ala
	-5					1				5					
Gly	Arg	Glu	Glu	Ile	Ala	His	Ser	Ile	Gln	Thr	Leu	Leu	Asp	Asp	Ala
10				15					20						25
Thr	Glu	Leu	Trp	Gly	Ile	Arg	Val	Ala	Arg	Val	Glu	Ile	Lys	Asp	Val
			30					35						40	
Arg	Ile	Pro	Val	Gln	Leu	Gln	Arg	Ser	Met	Ala	Ala	Glu	Ala	Glu	Ala
		45					50					55			
Thr	Arg	Glu	Ala	Arg	Ala	Lys	Val	Leu	Ala	Ala	Glu	Gly	Glu	Met	Asn
	60					65					70				
Ala	Ser	Lys	Ser	Leu	Lys	Ser	Ala	Ser	Met	Val	Leu	Ala	Glu	Ser	Pro
	75					80					85				

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Ile Ala Leu Gln Leu Arg Tyr Leu Gln Thr Leu Ser Thr Val Ala Thr
 90 95 100 105
 Glu Lys Asn Ser Thr Ile Val Phe Pro Leu Pro Met Asn Ile Leu Glu
 110 115 120
 Gly Ile Gly Gly Val Ser Tyr Asp Asn His Lys Lys Leu Pro Asn Lys
 125 130 135
 Ala

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 cta aca gaa aag ctg agg aaa ttc cgc ttc cga aaa gag aca gac aat 97
 Leu Thr Glu Lys Leu Arg Lys Phe Arg Phe Arg Lys Glu Thr Asp Asn
 15 20 25
 gca gcc atc ata atg aag gtg gac aaa gac cgg cag atg gtg gtg ctg 145
 Ala Ala Ile Ile Met Lys Val Asp Lys Asp Arg Gln Met Val Val Leu
 30 35 40 45
 gag gaa gaa ttt cgg aac att tcc cca gag gag ctc aaa atg gag ttg 193
 Glu Glu Glu Phe Arg Asn Ile Ser Pro Glu Glu Leu Lys Met Glu Leu
 50 55 60
 ccg gag aga cag ccc agg ttc gtg gtt tac agc tac aag tac gtg cgt 241
 Pro Glu Arg Gln Pro Arg Phe Val Val Tyr Ser Tyr Lys Tyr Val Arg
 65 70 75
 gac gat ggc cga gtg tcc tac cct ttg tgt ttc atc ttc tcc agc cct 289
 Asp Asp Gly Arg Val Ser Tyr Pro Leu Cys Phe Ile Phe Ser Ser Pro
 80 85 90
 gtg ggc tgc aag ccg gaa caa cag atg atg tat gca ggg agt aaa aac 337
 Val Gly Cys Lys Pro Glu Gln Gln Met Met Tyr Ala Gly Ser Lys Asn
 95 100 105
 agg ctg gtg cag aca gca gag ctc aca aag gtg ttc gaa atc cgc acc 385
 Arg Leu Val Gln Thr Ala Glu Leu Thr Lys Val Phe Glu Ile Arg Thr
 110 115 120 125
 act gat gac ctc act gag gcc tgg ctc caa gaa aag ttg tct ttc ttt 433
 Thr Asp Asp Leu Thr Glu Ala Trp Leu Gln Glu Lys Leu Ser Phe Phe
 130 135 140
 cgt tga tctctgggct ggggactgaa ttctgatgt ctgagtcctc aagggtgactg 489
 Arg
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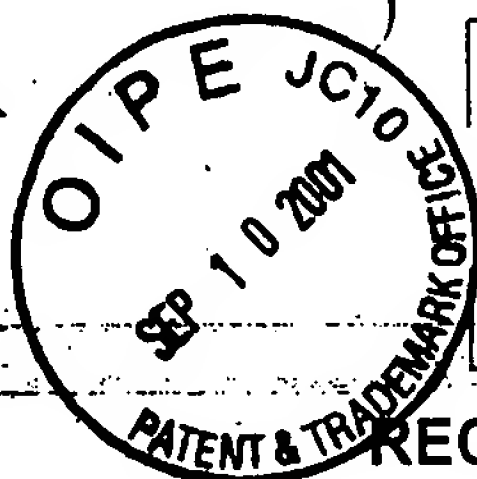
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340

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Met	Ser	Asp	Ser	Leu	Val	Val	Cys	Glu	Val	Asp	Pro	Glu	Leu	Thr	Glu	
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Lys	Leu	Arg	Lys	Phe	Arg	Phe	Arg	Lys	Glu	Thr	Asp	Asn	Ala	Ala	Ile	
			20					25					30			
Ile	Met	Lys	Val	Asp	Lys	Asp	Arg	Gln	Met	Val	Val	Leu	Glu	Glu	Glu	
			35				40					45				
Phe	Arg	Asn	Ile	Ser	Pro	Glu	Glu	Leu	Lys	Met	Glu	Leu	Pro	Glu	Arg	
	50					55				60						
Gln	Pro	Arg	Phe	Val	Val	Tyr	Ser	Tyr	Lys	Tyr	Val	Arg	Asp	Asp	Gly	
65					70				75						80	
Arg	Val	Ser	Tyr	Pro	Leu	Cys	Phe	Ile	Phe	Ser	Ser	Pro	Val	Gly	Cys	
			85					90						95		
Lys	Pro	Glu	Gln	Gln	Met	Met	Tyr	Ala	Gly	Ser	Lys	Asn	Arg	Leu	Val	
			100					105					110			
Gln	Thr	Ala	Glu	Leu	Thr	Lys	Val	Phe	Glu	Ile	Arg	Thr	Thr	Asp	Asp	
		115					120					125				
Leu	Thr	Glu	Ala	Trp	Leu	Gln	Glu	Lys	Leu	Ser	Phe	Phe	Arg			
	130					135							140			

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1-858-597-2600

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3

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Patent Application Number(s)

09/663,600

Patent Number(s)

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Name (line 1) Aymeric Duclert

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